

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 55

TO: Janet Epps-Ford

Location: REM-2C05&2C70

Art Unit: 1633

Wednesday, August 03, 2005

Case Serial Number: 09/489079

From: Deirdre Arnold

Location: Biotech-Chem Library

REM 1A64

Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards,
Deirdre Arnold



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Wed Aug 3 07:56:03 2005
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    protein search, using sw model

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"Identification of a Tissue-specific Putative Transcription Factor in Breast Tissue by Serological Screening of a Breast Cancer Library."; Cancer Res. 61:2055-2061(2001).
EMBL: AF269098; AMK27326.1; -.
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                                                                                       832 KSVPNKALELKNEQTLRADOMFPSESKOKKVBENSWDSESLRETVSOKDVCVPKATHOKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 49.2%; Pred. No. 2.3e-48; Conservative 57; Mismatches 89; Indels 106; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Breast cancer antigen NY-BR-1.1 (Fragment).
                                                                                                                                                                                                                                 385
                                                                                                                                                                                                                                                        952 EIKSQLENQKVKWEQELCSVR-LTL 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50088; ANK REPEAT; 1.
PROSITE; PS50297; ANK REP REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=21174979; Pubmed=11280766;
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Matches 244; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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SMART; SM00248; ANK; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                          326 RARELOKUHCEQCTGKMEQMKKKFCVLKKKLSEAKEIKSQLENOKVKWEQELCSVRF--- 382
                                                                                                                                                                                                         805 RGRELKKONCEQITAKWEQMKNKFCVLQKELSEAKEIKSQLENQKAKWEQELCSVRLPLN 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 LPKAAHQKEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKALELMD-----MQTFKAEPP 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 EKPSAFEPAIEMQKSVPNKALELKNEQTLRADE-ILPSESKQKDYEESSWDSESLCETVS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ::: | | | ::: | | ::: | | ::: | | ::: | ERYLHLKPTIEMKDSVPNKAGGMKDVQTSKAAEHDLEVASEEEQEREGSENNQPQVEEER 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    612 GPALQMKEVKSTEKEKRTSKESVNSPVFGKASLLTGGLLQVDDDSSLSEIDEDEGRPTKK 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --ALELMDMQ-TFKAEPPEKPSAFEPAIEMQKSVPNKALELKNEQTLR---ADQMFPS-- 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPNKALELKNEQTL------RADEILPSESKQKDYEESSWDSESLCETVSQKDV-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KK-----HRNNEMEVSANIHDGATDDAEDDDDDGLIQKRKSGETDHQQFPRKENKEYAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kikuno R., Nagase T., Ishikawa K., Hirosawa M., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIV.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 6:197-205(1999).
BMBL; ABO28997; BAA83026.2; -.
InterPro, IPR002110; ANK.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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al Similarity 30.4%; Pred. No. 2.3e-10;
130; Conservative 77; Mismatches 160; Indels 6
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0-1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAX-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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PROSITE; PS50297; ANK REP REGION; 1.
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MEDLINE=99397452; PubMed=10470851;
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Last sequence update)
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Q9NS19;
01-OCT-2000 (TEMBLrel. 15,
01-OCT-2000 (TEMBLrel. 15,
01-JUN-2001 (TEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 27.7
Matches 109, Conservative
                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
                                                                                                                                                  PRELIMINARY;
375 QELCSVRF 382
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786 RELCSLRF
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SEQUENCE
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Q15694
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                                                                                    375
                                                                                                           377 IESAPLEQTINDULTYVDEVHKNRSDWMSALGLGQEEDIESPWDSESISENFPQKYVDP 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 QKDVCLPKATHQKEI-----DKINGKLESPDNDGFL---KAPCRMKVSIPTK----- 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            551 KK-----HRNNEMBVSANIHDGATDDAEDDDDDGLIQKRKSGETDHQQFPRKENKEYAS 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 ---ALELMDMQ-TFKAEPPEKPSAFEPAIEMQKSVPNKALELKNEQTLR---ADQMFPS- 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           606 SGPALQMKEVKSTEKEKRTSKESVNSPVFGKASLLITGGLLQVDDDSSLSEIDEDEGRPTK 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 ----ESKQKOVVEENSWDSESIRET--VSQKDVCVPKATHQKEM---DKISGKLEDSTSL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           666 KISNEKNKVKNQIQSMDDVDDLIQSSETASEDCELPHSSYKNFMLLIEQLGMECKDSVSL 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKILDTIHSCERARELOKDHCEQCTGKMEQMKKKFCVLKKKLSEAKEIKSQLENQKVKWE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ESKOKOVVEENSWDSESLRET--VSOKDVCVPKATHQKEM---DKISGKLEDSTSLS 315
                                           731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 VPNKALELKNEQTL------RADEILPSESKQKDYEESSWDSESLCETVSQKDV-C 53
                         TSNEKNKVKNQIQSMDDVDDLTQSSETASEDCELPHSSYKNFMLLIEQLGMECKDSVSLL
                                                                                    KILDTIHSCERARELQKDHCEQCTGKMEQMKKKFCVLKKKLSEAKEIKSQLENQKVKWEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437 LAGAADGKEKNIGNEQAE----DVFYIPSC-MSGSRNFKMAKLEDTRNVGMPVAHMESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.0%; Score 368.5; DB 2; Length 1710; 30.4%; Pred. No. 2.4e-10; tive 77; Mismatches 160; Indels 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE , 1710 AA; 196409 MW; 01CBF9BADB894872 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bird C.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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PROSITE; PS50297; ANK REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                               Created)
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01-MAR-2004 (TEEMBLEEL 16,
01-MAR-2004 (TEEMBLEEL 26,
BA145E8.1 (KIAA1074).
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HSSP; P20749; 1K1B.
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Pfam; PF00023; Ank; 4.
PRINTS; PR01415; ANKYRIN.
SMART; SM00248; ANK; 4.
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ELCSLRF 798
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Best Local Similarity
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76 KDGLLKANCGMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEMQKSVPNKALELKNEQ 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 QSAQKVIFKKKVSLLNIATRITGGWKSGTEYPENLPTLKATIENKNSVLNTATKMKDVQT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | : | : | : | : STPEQDLEMASEGEQKRLEEYENNQPQVKNQIHSRDDLDDIIQSSQTVSEDGDSLCCNCK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 -----MDKISGKLEDSTSLSKILDTIHSCERARELQKDHCEQCTGKMEQMKKKFCVLKKK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 NVILLIDQHEMKCKDCVHLLKIKKTFCLCKRLTELKDNHCEQLRVKIRKLKNKASVLQKR 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 -----IRGTVSSQR------QPALKATGDEKDSVSNIAREIKDGEK-SGTV--SPQK 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 DGFLKAPCRMKVSIPTKALBLMDMQTFKABPPEKPSAFBPAIEMQKSVPNKALBLKNEQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in tumor-induced
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Proc. Assoc. Am. Physicians 107:296-305(1995).
EMBL; U28831; AAB02177.1; -.
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0008200; F:ion channel inhibitor activity; NAS.
GO; GO:0030319; P:do: channel inhibitor activity NAS.
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.9%; Score 306; DB 2; Length 381; 27.7%; Pred. No. 6e-08; ive 69; Mismatches 174; Indels
                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Protein immuno-reactive with anti-PTH polyclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96187433; PubMed=8608414;
Kumar R., Haugen J.D., Wieben B.D., Londowski J.M., Cai
"Inhibitors of renal epithelial phosphate transport in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 AA; 42574 MW; BFE144AB3A21C6DD CRC64;
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381 AA
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Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                           rissum=uterus;
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TISSUEBERIA, and Uterus;

TISSUEBERIA, and Uterus;

MEDLINE=2238825; PubMed=1247932; DOI=10.1073/pnas.242603899;

A StraubBerg R.D., Collins F.S., Wagner L.H., Derge J.G.,

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A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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Raywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 DSTSLSKILDTIHSCERARELQKDHCEQCTGKMEQMKKKFCVLKKKLSEAKEIKSQLENQ 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DSTILSKILDAVPSCERGKELKKUHCEQITAKMEQTKNKFCVLQKELSEAKEIKSQLENQ 61
                                                                                                                   Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.S., Toyoda A., Ishii K., Totoki Y., Choi D.K., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechechmidt K., Polley A., Tandien S., Blechechmidt K., Polley A., Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S., Shimizu N., Sabaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P., Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H., Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., Lehrach H., Reinhardt R., Yaspo M.L., Submitted (MAY-2000) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                   Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                   14.8%; Score 303; DB 2; 72.3%; Pred. No. 9.6e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 60; Conservative
   PRED4 protein (Fragment)
Name=PRED4;
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                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                           SEQUENCE FROM N.A.
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82 RCKKDGEKTR---RVSSHKQPSLKATSDKEDSVPNMATETKDEQISGTVSCQKQPALKAT 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 DSESICETVSQXDVCLPKATHQXEIDKINGKLEESPDNDGFLKAPCRMKVSIPTKALELM 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 RRPALKTIGDEKDSVSNIAREIKDGEK-SGTV--SPQKQSAQKVIFKKKVSLLNIATRIT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 SWDSESLRETVSQK----DVCVPKATHQKE--------MDKISGKLEDSTSLSK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 ENNQPQVKNQIHSRDDLDDIIQSSQTVSEDGDSLCCNCKNVILLIDQHEMKCKDCVHLLK 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 AHQKEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKALELMDMQTFKAEPPEKPSAFEPA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 DMQTFKAEPPEKPSAFEPAIEMQKSVPNKALELKNEQT---LRADQMFPSESKQKNVEEN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 OKSVPNKALELKNEQTLRADEILPSESKOKDYEESSWDS----ESLCETVSQKDVCLPKA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 QKPPALKATSVKE-----DSVLNIAREKKOGEKSRTVSFEQPPGLKATRDEKDSLLNIA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Gaps
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Hymo sapiens (Human).
Eukaryota; Metazoma; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.8%; Score 282.5; DB 2; Length 450; 26.6%; Pred. No. 1.1e-06; Live 70; Mismatches 191; Indels 57.
                                                                                                                                                                                                                                                                                                                           Director MGC Project,
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0448H4 AAH44444.1; -.
EMBL; BC0318B3; AAH318B3.1; -.
                                                                                                                                                                                                Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450 AA; 50273 MW; 349C9AFCA2CBB6B5 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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05-JUL-2004 (TrEMBLrel. 27, Created)
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LCSLRFAIQQEKK 448
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Matches 115; Conservative
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                                                                                                SEQUENCE FROM N.A.
TISSUE=Brain;
Director MGC Project;
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1322 EKKKADEVK-KAEEKKKADELKKSEEKKKADELKKSEEKKKADELKKKAEEKKKADELKK 1380
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SEQUENCE FROM N.A.
MEDLINE=22072559; PubMed=12076768; DOI=10.1016/S0166-6851(02)00067-1;
Blair P.L., Kappe S.H., Maciel J.E., Balu B., Adams J.H.;
"Plasmodium falciparum MAEBL is a unique member of the ebl family.";
Mol. Biochem. Parasitol. 122:35-44(2002).
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                                                                                                                                                                                                                                                                                                 BLQKDHCEQCTGKMEQMKKKFCVLKKKLSEAKBIKSQLENQKVKWEQELCSVRFLTLMKM
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                                                                                 229 KPSAFEPALEMQKSVPNKALELKNEQTLRADQ--MFPSESKQKNVEENSWDSESLRETVS
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blair B.L., Kappe S.H.I., Maciel J.E., Balu D.J., Adams Esubmitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY042084; AAQ73469-1.; -
Interpro. IPR008602; Duffty_binding.
Pfam; PP05424; Duffty_binding.
SEQUENCE 2006 AA; 237620 MW; EE75EF42E2BF767D CRC64;
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MEDLINE=22077637; PubMed=12082132;
Michon P., Stevens J.R., Kaneko O., Adams J.H.;
"Evolutionary relationships of conserved cysteine-rich adhesive molecules of malaria parasites.";
Mol. Biol. Evol. 19:1128-1142(2002).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Bythrocyte binding protein 3.
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hes 109; Conservative
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Q7K5Q6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 KATHQKEM---DKISGKLEDSTSLSKILDTIHSCERARELQKOHCEQCTGKMEQMKKKFC 350
                                                                                                                                                                                                                                                                                                                                                                                        87 KVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEMQKSVPNKALELKNEQTLRADEILPSE 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                              66
  Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kifunci K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagateuma M., Takahabhi-Piji A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AK128577; BAC87508.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 L---KAPCRMKVSIPTK-----ALBLMOMQ-TFKAEPPEKPSAFEPAIEMQKSVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 SKOKDYEESSWDSESLCETVSOKDVCLPKATHOKEIDKINGKL------EESPDNDGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                              KVSLKEBLQQ--DMQRFKNE-----IGMLK-VEFQALBKEKVQL-----
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                           13.1%; Score 268.5; DB 2; Length 1080; 28.0%; Pred. No. 1.4e-05; ive 62; Mismatches 96; Indels 81;
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                                                                                                                                                                                                                              1080 AA; 126741 MW; 47BBAAA933AE595C CRC64;
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DNA Res. 7:273-281(2000).
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01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2002 (TrEMBLrel. 22,
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                                                                                                                                                                                                                                                                                                                                         93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angluoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McRadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Praser C.M., Barrell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 KALELKN-EQTLRADEILPSESKQKDYE----ESSWDSESLCETVSQK---DVCLPKAA
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                                                                                                                                 1594 EEEEKIKAEOLKKEEEEKKKVEOLKKKEEEEKKKAEOLKKEEEENKIKAEO 1644
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                                                                               ---AKEIKSQLENQKVKWEQ
                                                                                                                                                                                                                                                                                                                                                                                                                         ORFNames=PF11 0486;
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the human malaria parasite Plasmodium
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro: IPRO08602; Duffty_binding.
Pfam; PF05424; Duffy_binding. 1.
SEQUENCE 2055 AA; 243211 MW; 783F48BB7286B1F3 CRC64;
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  Last sequence update)
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al Similarity 26.5%; Pred. No. 0.002;
109; Conservative 65; Mismatches 166;
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                                                                               DHCEQCTG----KMEQMKKKFCVLKKKLSE-
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EMBL; AE014843; AAN36066.1; -.
HSSP; P04268; 11C2.
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                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                             1487 EKKKADELKKABEKKKADELKKAEEKKKADELKKAEEKKKADELKKAEELKKAEKKKVE 1546
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                              PPEKPSAFEPAIEMQKS-----SVPNKALELKN-EQTLRADQMFPSE----SKQKNVF 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] SEQUENCE FROM N.A. MEDICAL DOI=10.1016/S0166-6851(02)00067-1; MEDLINE=22072559; Pubmed=12076768; DOI=10.1016/S0166-6851(02)00067-1; BABIT P.L., Kappe S.H., Maciel J.E., Balu B., Adams J.H.; Plasmodium falciparum MABBI is a unique member of the ebl family."; Mol. Biochem. Parasitol. 122:35-44(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2019;
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MEDLINE=22077637; PubMed=12082132;
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(TrEMBLrel. 27, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S., Okazaki N., Kikuno R.F., Ohara M., Kaisho T., Hoshino K., Kitamura H., Nagase T., Ohara O., Koga H.;

"Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: IV. The Complete Nuclectide Sequences of 500 Mouse KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 KAPCRMKVS---IPTKALBLM----DMOTFKAEPPEKPSAFEPAIEMOKSVPNKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 ELKNEQTLRADQM----PPSESKQKNVBENSWDSESLRETVSQKDVCVPKATHQKEMDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 SGKLEDSTSLSKILDTIHSCERARELQXDHCEQCTGKMEQMKKKFCVLKKKLSEAKEIKS
                                                                                     ----KAEOLKK
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                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                         333 DHCEQCTG----KMEQMKKKFCVLKKKLSE----AKEIKSQLENQKVKWEQ 375
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                                                                          1043 AA; 121354 MW; 5F37B1F9AA37B212 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
4) Hypothetical protein DKFZp6666M032 (Fragment).
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Last sequence update)
Last annotation update)
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31.3%; Pred. No. 0.0034;
iive 37; Mismatches 54;
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Interpro; IPR009054; Topismrse_insert.
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Mammalia, Eutheria, Rodentia,
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Name=mKIAA1074;
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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                                                                                                                                                                                                                                                                                                                                   MEDLINE=22072559; PubMed=12076768; DOI=10.1016/S0166-6851(02)00067-1; Blair P.L., Kappe S.H., Maciel J.E., Balu B., Adams J.H.; "Plasmodium falciparum MAEBL is a unique member of the ebl family."; Mol. Biochem. Parasitol. 122:35-44(2002).
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     BEBEKIKAEQLKKEBEBEKKKVEQLKKKEBEBEKKKAEQLKKEBEBINITAEQ 1644
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"Brodultionarry relationships of conserved cysteine-rich motifs adhesive molecules of malaria parasites.";
Mol. Biol. Evol. 19:1128-1142 (2002).
                                                                                                                                                             Last sequence update)
Last annotation update)
1 (Chimeric erythrocyte-binding
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPRO08602; Duffy binding.
Pfam; PF05424; Duffy binding.
SEQUENCE 2055 AA; 243211 MW; 783F48BB7286B1F3 CRC64;
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65; Mismatches 166;
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05-JUL-2004
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                                                                                                                                                                            SEQUENCE FROM N.A.

TISSUE-Stomach;
The German cDNA Consortium;
Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
BMBL, AL832977; CAH56324.1; -.
Hypothetical protein.
NON TER 308
SEQÜENCE 308 AA; 34328 MW; DC3BDC42DC587AF3 CRC64;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
10.5%; Score 214.5; DB 2; Length 308;
Best Local Similarity 26.4%; Pred. No. 0.0018;
Matches 86; Conservative 54; Mismatches 147; Indels 39
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Homo sapiens (human)
JP 2002540761-A/8
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PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
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1. (bases 1 to 2683)
Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Russell,J.C. and Stroupe,S.D.
Russell,J.C. and Stroupe,S.D.
Rasgente and methods useful for detecting diseases of the breast Patent: JP 2002540761-A 8 03-DEC-2002;
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JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL
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AR561904
AR561904
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AR454006
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-DB-GGenEmbl -OFWT=fastap -GUPFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=hunan40.cdi -LIST=45
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-UNITS=bits -START=1 -END=-1 -MATRIX=100 -TMR MIN=0 -ALIGN=15 -MODE=LOCAL
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-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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BD271312 Reagents
AR283468 Sequence
AR454017 Sequence
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                  OM protein - nucleic search, using frame_plus_p2n model
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E (Dases 1 to 2683)

E (Dases 1 to 2683)

Medel, P.A. B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
Russell, J.C. and Stroupe, S.D.
Reagents and methods useful for detecting diseases of the breast patent: JP 2002540761-A 9 03-DEC-2002;
ABBOTT LABORATORIES
OS Homo sapiens (human)
PN JP 2002540761-A/9
PP 31-JAN-1999 US 09/234716
PR 21-JAN-1999 US 09/234716
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
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JP 2002540761-A/9
03-DEC-2002
21-JAN-1999 US 09/224716
PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
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Reagents and methods useful for detecting diseases of the CC breast
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957 ATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTATCAAAAATCTTGGATACA
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Reagents and methods useful for detecting diseases of
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FT / Organism='Homo sapiens (human)'. FEATURES 1. 2683 1. 2683 1. 2683 1. 2683 1. 2683 1. 2683 1. 2683 1. 2683 1. 2683 1. 2683 1. 2683 1. 2016 1. 201	Alignment Scores: 2.8e-165 Length: 2683 Pred. No.: 2052.00 Matches: 398 Score: 2052.00 Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 6 Gaps: 0	US-09-489-079-24 (1-398) x BD271312 (1-2683) Qy		Qy 41 GluserLeuCysGluThrValSerGlnLysAspValCysLeuProLysAlaAlaHisGln 60 Db 177 GAGAGTCTCTGTGAGACTGTTTCACAGAAGATGTGTGTTTACCCAAGGCTGCGCATCAA 236	Oy 61 LysGlulleAspLysIleAsnGlyLysLeuGluGlySerProValLysAspGlyLeuLeu 80 	Qy 81 LysalaasnCysGlyMetLysValSexIleProThrLysAlaLeuGluLeuMetAspMet 100	101 GINThrPheLygalaGluProProGluLysProSerAlaPheGluProAlaIleGluMet 120 	121 GlniyaSerValProAsniyaAlaLeuGluLeuLyBAsnGluGlnThrLeuArgAlaAsp 140 	141 GluileLeuProSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGlu 160 	161 SerLeuCysGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGlnLys 180 	Oy 181 GluileaspiysileasnglyiysieuglugluserProaspashaspglyPheLeuiys 200	Oy 201 AlabroCysArgMetLysValSerIleProThrLysAlaleuGluLeuMetAspMetGln 220		241 LysSerValProhsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGln 260 	261 MetPheProSerGluSerLygGlnLygAsnValGluGluAsnSerTrpAspSerGluSer 280

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Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L.,
Hepler, W.T. and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of b
cancer
Patent: US 6680197-A 491 20-JAN-2004;
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                                                                                               Location/Qualifiers
1. .2232
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/organism="unknown"
/mol_type="genomic DNA"
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                                                                            Unclassified.
1 (Dasses 1 to 3681)
Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L. and
Hepler,W.T.
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Matches:
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Location/Qualifiers
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          AR283451 3681 bp D1
Seguence 463 from patent US 6528054.
AR283451
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                   1968 ACTITCAAAGCAGAGCCICCCGAGAAGCCAICIGCCTICGAGCCTGCCATIGAAAIGCAA
                                                              LysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGln
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Yuqiu, J., Dillon, D.C., Mitcham, J.L., Xu, J. and Harlocker, S.L. Compositions for the treatment and diagnosis of breast cancer methods for their use patent: US 6579973-A 463 17-JUN-2003;
Location/Qualifiers
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Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L.
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Hepler,W.T.
Compositions and methods for the therapy
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                                                                US 6586572.
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Location/Qualifiers
1. 3681
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Sequence 463 from patent
AR351420
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                                                           GAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTTACCCAAGGCTRCRCATCAA
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     AspGlulleLeuProSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSer
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GAAATAGATAAAATAAAATTAGAAGACTCTCCTGATAATGATGGTTTTCTGAAG 1907	AAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAAACA			ArgPheLeuThrLeuwetlysMetLysIleileSerTyrWetLysIleAlaCys 398 	3681 bp DNA linear PAT 20-FEB-2004 t US 6680197.	, Mitcham,J.L., Xu,J., Harlocker,S.L., erson,R.A.	3 20-JAN-2004; fiers nown" omic DNA"	Length: 3681 Matches: 393 Conservative: 1 Mismatches: 4 Indels: 0 Gaps: 0
GAAA AlaP ACTT ACTT	2028 AAGTCTGTTCCAAATAAAGCC 261 MetPheProSerGluSerLy8 2088 ATGTTCCCTTCAGAATCAAAA 281 LeuargGluThrValSerGln 2148 CTCCTGAGACTCACAA	301 MetasplysileserGlylys	341 LysMetGluGlnMetLysLys 2328 AAATGGAACAATGAAAAG 361 GluIleLysSerGlnLeuGlu 2388 GAAATAAAATCACGTTAGAG	381 ArgPheLeuThrLeuMetLys 	AR454000 Sequence 463 from patent AR454000 AR454000.1 GI:42686790 Unknown.	Unknown. Unclassified. 1 (bases 1 to 3681) Jiang,Y., Dillon,D.C., Mit Hepler,W.T. and Henderson, Compositions and methods f	Patent: US 6680197-A 463 20-JAN-; Location/Qualifiers 13681 /organism="unknown" /mol_type="genomic DNA"	Scores: 1.2e-162 2023.00 milarity: 98.99% Similarity: 98.59% in: 6 079-24 (1-398) x AR454000
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11	RESULT 12 AX303143 AX303143 LOCUS LOCUS Sequence 463 from Patent W00179286. ACCESSION VERSION VERSION VERSION VERYWORDS SOURCE ORGANISM Homo sapiens CORGANISM AX303143 CORGANISM Homo sapiens CORGANISM Homo sapiens CORGANISM AX303143 CORGANISM CORGANISM CORGANISM AX303143 CORGANISM CORGANISM CORGANISM AX303143 CORGANISM CORGANISM CORGANISM AX303143 CORGANISM	ent Scores: t Similarity: ccal Similarity: acth: 1 MetGl: 1308 ATGCAL 21 ASpGl: 1368 GATGAL 1428 GAGAG 61 LysGl: 1548 AAGGAG 1548 AAGGAG 11548 AAG
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Patent: US 6528054-A 490 04-MAR-2003;

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-LIGN=FAS_DOCAHIGN=200 -THE SCORE-PGC -THE MAX=100 -THE MIN=0 -ALIGN=15
-MODEL=LOCAL_OUTFMT=DCO -UNGRM=ext -HEAPESTEE=500 -MINLEN=0 -MAXIEN=200000000
-USER=US09489079_GCGN 1_1 1418_Grunat_01082005_141249_13290 -NCPU=6 -ICPU=3
-NO_WMAP_LARGEQUERY_NEG_SCORES=0 -WAIT -BSPBGCK=100 -LONGINGG
-DSW_TIMEOUT=120 -WARN TIMEOUT=30 -THERDSO=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPOR=1 - YGAPOP=10 -YGAPOP=0.5 -DELOP=6 -DELEXT=7
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Aaa59014 Nucleotid
Aas47405 Human cDN
Aas47422 Human cDN
Abs64023 Human bre
                                                                             August 1, 2005, 22:23:28; Search time 737.055 Seconds (without alignments) 3196.585 Million cell updates/sec
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1 MQKSVPNKALELKNEQTLRA.....SVRFLTLMKMKIISYMKIAC 398
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                GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                          - nucleic search, using frame_plus_p2n model
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AlabroCysArgMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGln
                 GCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAGCCTTAGAATTGATGGACATGCAA
                                                                     LeuArgGluThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGlu
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                                                        ThrPheLysAlaGluProProGluLysProSerAlaPheGluProAlaIleGluMetGln
                                                                                                           LysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGln
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Granados EN, Hodges SC, Klass MR, Kratochvil JD, Russell JC;
Stroupe SD;
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                                                                                                                                                                                                        The present sequence encodes a human BS322 polypeptide. BS322 is a breast tissue marker. The BS322 polynuclectides and polypeptides are used to detect and diagnose breast disease, e.g. breast cancer. The BS322 polynuclectides are useful as a source of probes and primers, and the BS322 polypeptides are useful as antigens
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                                           Cohen M, Colpitts TL, Friedman PN, Gordon on SC, Klass MR, Kratochvil JD, Russell JC;
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Gaps:
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                                                                                                                                                                                 Claim 12; Page 119-120; 126pp; English
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P-PSDB; AAB07638, AAB07639.
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                 (ABBO ) ABBOTT
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Granados EN,
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                                                                      Stroupe SD;
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                                                                                                                                                                               LysMetGluGlnMetLysLysPheCysValLeuLysLysLysLeuSerGluAlaLys
                                                           CTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTGTACCCAAGGCTACACATCAAAAAGAA
                                                                                                                                  | IleHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnCysThrGly
                                                                                                                                                  GAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAACAAGAGGCTCTGCAGTGTG
MetPheProSerGluSerLysGlnLysAsnValGluGluAsnSerTrpAspSerGluSer
                  ATGTTCCCTTCAGAATCAAAACAAAGAACGTTCAAAAAAATTCTTGGGATTCTGAGAG
                                           LeultgGluThrValSerGlnLygAspValCygValProLygAlaThrHisGlnLygGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                cancer protein; tumour; cancer; cytostatic,
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22-JUN-2000; 2000US-00604287.
20-JUL-2000; 2000US-00620405.
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                        The present sequence represents the full length cDNA sequence encoding BS322 polypeptide. BS322 is a breast tissue marker. The BS322 polymorlectides and polymorpatides are used to detect and diagnose breast disease, e.g. breast cancer. The BS322 polymuclectides are useful as a source of probes and primers, and the BS322 polypeptides are useful as
                                                                                                                                                                                                                                                                                                                                GluileLeuProSerGluSerLysGluLysAspTyrGluGluSerTrpAspSerGlu
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                                                                                                                                                                                                                                                                                       21 AspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSer
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Matches:
Conservative:
Mismatches:
Indels:
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     Page 118-119; 126pp; English
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                                                                                                                                        1.94e-176
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100.00%
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Best Local Similarity: 1
Query Match:
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1968 ACTITICAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAGCCTGCCATTGAAATGCAA 2027
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                       LysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGln 260
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                                     2028 AAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAACAACATGAGAGCAGATCAG
                                                                                   2088 AIGTICCCTICAGAAICAAAAGAAAGAAAGITGAAGAAAITCTIGGGAITCTGAGAGI
                                                                                                                                    2148 CTCCGTGAGACTGTTTCACAGAAGGATGTGTGTGTGTACCCAAGGCTACACATCAACAAAAAAA
                                                                                                                                                                   MetAsplys1leSerGlyLysLeuGluAspSerThrSerLeuSerLys1leLeuAspThr
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                                                                      MetPheProSerGluSerLysGlnLysAsnValGluGluAsnSerTrpAspSerGluSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA encoding breast cancer protein B726P fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; 88; breast cancer protein; tumour; cancer; cytostatic;
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08-JUN-2000; 2000US-00590751.
22-JUN-2000; 2000US-00604287.
20-JUL-2000; 2000US-00620405.
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P-PSDB; AAU33358.
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Also included are expression vectors expressing the proteins, transformed cells and antibodies raised against the proteins or an antigen presenting cells and antibodies raised against the proteins or an antigen presenting cells and antibodies raised against the proteins or an antigen presenting in the prevention, diagnosis and treatment of diseases associated with inappropriate breast tumour protein expression, i.e. breast tumours and complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids and their complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The proteins, nucleic acids and antibodies may be used to down requiste expression and activity. The antibodies may also be used to down requist expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immunocorpant assay (ELISA) and in other immunocorpant and encodes a breast tumour protein of the
including immunogenic fragments of the proteins
   encode them,
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Sequence 2232 BP; 826 A; 399 C; 467 G; 535 T; 0 U; 5 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 6.63e-174 2023.00 98.99% 98.74% 98.59% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB:

US-09-489-079-24 (1-398) x AAS47422 (1-2232)

1155 1095 40 9 80 MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla LysGlulleAspLysIleAsnGlyLysLeuGluGlySerProValLysAspGlyLeuLeu AspGlulleLeuProSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSer GATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAAAGTTCTTGGGATTCT GluSerLeuCysGluThrValSerGlnLysAspValCysLeuProLysAlaAlaHisGln 1096 1156 21 41 61 g g 名 ઠે ઠ 8 Š

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GlulleAspLyslleAsnGlyLysLeuGluGluSerProAspAsnAspGlyPheLeuLys

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2115 2175 1995 1935 2055 AAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAACAATGAGAGCAGATCAG 1815 260 300 320 340 360 380 LysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGln LeuargGluThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGlu 201 AlaProCysArgMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGln Met Phe ProSerGluSerLysGlnLysAsnValGluGluAsnSerTrpAspSerGluSer 321 IleHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnCysThrGly 341 LysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLys 2056 AAAATGGAACAAATGAAAAAGAAGTTTTGTGTACTGAAAAAGAAACTGTCAGAAGCAAAA ThrPheLysAlaGluProProGluLysProSerAlaPheGluProAlaIleGluMetGln MetAsplysileSerGlyLysLeuGluAspSerThrSerLeuSerLysileLeuAspThr GluileiysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerVal 2176 AGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGCATGT 2229 381 ArgPheLeuThrLeuMetLy8MetLy811e11eSerTyrMetLy811eAlaCy8 361 2116 1636 1696 1756 1876 301 221 241 261 281 엄 셤 셤 셤 셤 à 요 ઠે 셤 ઠે g ठे g 8 8 8 ò Š Š

ABS64023 Btandard; DNA; 2232 BP ABS64023 RESULT

(first entry) 15-NOV-2002 ABS64023

Human; breast tumour protein; gene; ds; breast cancer; cytostatic; vaccine.

Human breast tumour polynucleotide #472.

Homo sapiens.

US2002085998-A1.

04-JUL-2002

2001US-00834759 28-DEC-1998; 02-APR-1999; 23-JUN-1999; 02-SEP-1999; 03-NOV-1999; 13-APR-2001;

980S-0022575. 990S-00385480. 990S-00339338. 990S-00433826. 2000US-00551621. 2000US-0059051. 08-JUN-2000; 17-APR-2000; 20-JUL-2000;

(CORI-) CORIXA CORP

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Fanger GR;
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tumour; breast cancer; cancer; immune response stimulation.
1696 ACTITICAAAGCAGAGCCTCCCGAGAAGCCATCTGCCTTCGAGCCTGCCATTGAAATGCAA

        MetPheProSerGluSerLysGlnLysAsnValGluGluAsnSerTrpAspSerGluSer

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Xu J, Harlocker SL, Hepler WT, Henderson RA,
Moneill PD, Durham M;
                                                          AlaproCysArgMetLysValSerIleProThrLysAlaLeuGluLeuMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tumour-related DNA sequence - SEQ ID No 491.
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07-DEC-2001; 2001US-00007805.
13-FEB-2002; 2002US-00076622.
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Vedvick TS,
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                                                                                                                                                                                                                The invention relates to an isolated breast tumour polynuclectide and the polypeptide it encodes. The polynuclectide and polypeptide are useful for detecting the presence of breast cancer in a patient, and in pharmaceutical compositions for treating breast cancer. The sequences are useful for stimulating an immune response in a patient and can therefore be used in production of vaccines. The sequences are also useful for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with a composition of the invention and detecting the amount of polynucleotide that hybridizes to the sample. This sequence represents a human breast tumour polynucleotide of the invention
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                                                                                                           Novel breast cancer polynucleotides and polypeptides encoded by the polynucleotides, useful for detecting the presence of breast cancer in a patient, and in pharmaceutical compositions, for treating breast cancer.
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ThrPheLysAlaGluProProGluLysProSerAlaPheGluProAlaIleGluMetGln
                                                       LysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGln
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03-NOV-1999;
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22-JUN-2000;
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                                                                                                         The invention comprises a method of stimulating and/or expanding T cells specific for a tumour protein. The invention further comprises human nucleic acids and proteins that are associated with tumours (e.g. breast cancer). The method and sequences of the invention are useful for stimulating and/or expanding T cells specific for a tumour protein, detecting the presence of cancer, stimulating an immune response in a patient and treating breast cancer. The present DNA sequence represents a human tumour-related DNA sequence.
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                               New polypeptide and polynucleotide useful for stimulating and/or expanding T cells specific for a tumor protein and treating breast
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                                                                                                             MetPheProSerGluSerLysGlnLysAsnValGluGluAsnSerTrpAspSerGluSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated polypeptide useful for the treatment and diagnosis of e.g. breast cancer comprises at least an immunogenic portion of a tumor protein.
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                                                                                                                                     The invention relates to an isolated breast cancer-associated polypeptide. The polypeptide may be used for the diagnosis and treatment of breast cancers. The methods are useful for detecting the presence of cancer in a patient and treating a cancer in a patient. The present sequence represents DNA encoding a human breast cancer-associated polypeptide fusion protein.
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                                                                   An isolated oncogenic polypeptide useful for preventing, diagnosing
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                                                                                                            Disclosure; SEQ ID NO 491; 294pp; English
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98.99%
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Sleath PR,
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Houghton
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DNA microarray analysis; polymerase chain reaction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying tissue (tumor)-specific polynucleotides overexpressed in tissue of interest as compared to control tissue, for detecting cancer cells in patient, comprises DNA microarray analysis or quantitative
                                                                                                                                                          LysMetGluGlnMetLysLysLysLysBeCysValLeuLysLysLysLeuSerGluAlaLys
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                                               MetAsplys1leSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeuAspThr
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                                                                                                                                                                                                                                                                                   AspGlulleLeuProSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSer
The present invention provides the coding sequences and some protein sequences of proteins associated with breast cancer in humans. These sequences can be used in the diagnosis and treatment of cancers, particularly breast tumours
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biological sample such as blood, serum, lymph nodes, bone marrow, sputum, urine or a tumour biopsy sample. The methods are useful for determining the presence or absence of or monitoring progression of prostate, breast, colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver, gastric, kidney, bladder, pancreatic or endometrial cancer. Sequences AAI67218-223 represent determined CDNA seqeunces of splice variants of
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LeuArgGluThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGlu
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23-JUN-1999; 99US-00339338.
03-NOV-1999; 99US-00338261.
03-NOV-1999; 99US-00433826.
17-APR-2000; 2000US-00551621.
22-JUN-2000; 2000US-00590751.
22-JUN-2000; 2000US-00664287.
20-JUL-2000; 2000US-00664287.
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Human tumour-related DNA sequence
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 polypeptide it encodes. The polynucleotide and polypeptide are useful for detecting the presence of breast cancer in a patient, and in pharmacutical compositions for treating breast cancer. The sequences are useful for stimulating an immune response in a patient and can therefore be used in production of vaccines. The sequences are also useful for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample a composition of the invention and detecting the amount of polynucleotide that hybridizes to the sample. This sequence represents a human breast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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tumour; breast cancer; cancer; immune response stimulation.
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Henderson RA,
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nading T cells specific for a tumor protein and treating
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Harlocker SL, Hepler WT,
I PD, Durham M;
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GlulleLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnLeuCysSerVal
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03-NOV-1999; 99US-00338261.
03-NOV-1999; 99US-00433826.
17-APR-2000; 2000US-00551621.
08-JUN-2000; 2000US-00590751.
22-JUN-2000; 2000US-0050405.
13-APR-2001; 200US-00834759.
07-DEC-2001; 200US-000834759.
13-FEB-2002; 2002US-00076622.
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stimulating and/or expanding T cells specific for a tumour protein, detecting the presence of cancer, stimulating an immune response in a patient and treating breast cancer. The present DNA sequence represents human tumour-related DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGAAATAGATAAAATAAATGGAAAAATTAGAAGGGTCTCCTGTTAAAAGATGGTCTTCTG
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The invention relates to an isolated breast cancer-associated polypeptide. The polypeptide may be used for the diagnosis and treatment of breast cancers. The methods are useful for detecting the presence of An isolated oncogenic polypeptide useful for preventing, diagnosing and treating breast cancer. GAAATAAAATCACAGTTAGAGAACCAAAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGT gene therapy; protein therapy; vaccine; breast cancer; cancer; human; ArgPheLeuThrLeuMetLysMetLysIleIleSerTyrMetLysIleAlaCys 398 AGGTTTCTCACACTCATGAAAATGAAAATTATCTCTTACATGAAAATTGCATGT cancer-associated polypeptide cDNA #458

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aaaatggaacaaatgaaagaagttttgtgtactgaaaagaaactgtcagaagcaaaa
                                            321 IleHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnCysThrGly
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cancer in a patient and treating a cancer in a patient. The present sequence represents cDNA encoding a human breast cancer-associated polypeptide.
                                              0 U; 6 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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The invention relates to an isolated polypeptide comprising at least an immunogenic portion of a breast tumour protein. The polymucleotide, its polypeptide, its antibody, a pharmaceutical composition comprising the fusion protein or the polymucleotide encoding it, a vaccine comprising the fusion protein or the polymucleotide encoding it, an isolated T cell population comprising T cells specific for a breast tumour protein, and
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human; 88; gene; breast tumour; cancer; vaccine; T cell stimulator;
T cell expander.
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tumour; breast
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method for removing tumour cells from a biological sample is useful for inhibiting the development of a cancer in a patient. The polypeptide is useful for stimulating and/or expanding T cells specific for a breast tumour protein. Stimulating and/or expanding T cells specific for a breast tumour protein is useful for inhibiting the development of a breast tumour protein is useful for inhibiting the development of a cancer in a patient. The method additionally involves the step of cloning at least one proliferated cell and then administering the cloned T cells to the patient. The present sequence represents a cDNA associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; T cell stimulation; T cell expansion;
                                                                       MetaspiysileSerGlyLysLeuGluaspSerThrSerLeuSerLysIleLeuAspThr
                                                                                                                                                                                           LysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLys
                                                                                                                                                                                                                                                     2088 ATGITCCCTTCAGAATCAAAAGAAAGGTTGAAGAAAGATGTTCTTGGGATTCTGAGGT
                                                        LeuArgGluThrValSerGlnLysAspValCysValProLysAlaThrHisGlnLysGlu
                                                                                                                             2388 GAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTG
MetPheProSerGluSerLysGlnLysAsnValGluGluAsnSerTrpAspSerGluSer
                                                                                                                                                                         321 IleHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnCysThrGly
                                                                                                                                                                                                                                                                                      GluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerVal
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                                                                                                                                                                                                                                                                                                                                                DC;
RA,
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, Henderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human tumour-related DNA sequence - SEQ ID No 549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Persing DH, Jiang )
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Xu J, Harlocker
Mcneill PD, Durh
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07-DEC-2001; 2001US-00007805.
13-FEB-2002; 2002US-00076622.
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The invention relates to an isolated breast cancer-associated polypeptide. The polypeptide may be used for the diagnosis and treatment of breast cancers. The methods are useful for detecting the presence of a cancer in a patient and treating a cancer in a patient. The present
                                                                                  321 IleHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnCysThrGly 340 ...
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                                                                                                                                                   AAAATGGAACAAAAAAAAAAAGAAGTTTTGTGTACTGAAAAAGAAACTGTCAGAAGCAAAA
                                                                                                                                                                                                        GAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTG
                                   MetAspLys11eSerGlyLysLeuGluAspSerThrSerLeuSerLys11eLeuAspThr
                                                                                                                                   LysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGluAlaLys
                                                                                                                                                                               Glu11eLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLeuCysSerVal
                                                                                                                                                                                                                             ArgPheleuThrLeuMetLysMetLysIlelleSerTyrMetLysIleAlaCys 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing
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                                                                                                                                                                                                                                                                                                                                                                          cancer-associated polypeptide cDNA #493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated oncogenic polypeptide useful for
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2000US-00590731.
2000US-006204087.
2000US-00834759.
2001US-00070805.
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99US-00285480.
99US-00339338.
99US-00389681.
99US-00433826.
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02-APR-1999;
23-UNN-1999;
03-SEP-1999;
03-NOV-1999;
17-APR-2000;
22-JUN-2000;
20-JUN-2000;
20-JUN-2000;
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07-DEC-2001; 2
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    detecting the presence of cancer, stimulating an immune response in a patient and treating breast cancer. The present DNA sequence represents human tumour-related DNA sequence
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                                                   Sequence 1953 BP; 745 A; 342 C; 411 G; 454 T; 0 U; 1 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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human breast cancer-associated
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Matches:
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sequence represents cDNA encoding polypeptide.
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                             1837 GAAATAAAATCACAGTTAGAGAACCAAAAAGTTAAATGGGAACAAGAGCTCTGCAGTGTG
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                                                                                                                                                                                                                                                                                                381 ArgPheLeuThrLeuMetLysMetLysIleIleSerTyrMetLysIleAlaCys 398
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RC1-BT025 AGENCOURT BP312630

Homo sapi 939288 MA AGENCOURT

Pan trogl CR735535

AST-T32E0 EST35833

UI-M-FYO-Ношо

Homo sapi RC1-BT025

ox78g05.x UI-CF-DU1 ic21c08.y df113d08.

UI-E-CK1-df113d08.

OM protein

Run on:

Sequence:

Searched:

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AA447146 zw93g02.8
BE929777 RC3-GN004
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CR627244 BU607446 BU607446 BMS40985 AA781851 CR731066
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IMAGE:4821910), containing frame-shift errors.
                        BP313822
BP313235
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 -MODEL-frame+ p2n.model -DEV-xlp
-MODEL-frame+ p2n.model -DEV-xlp
-MODEL-frame+ p2n.model -DEV-xlp
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-FGAPEXT=7 -YGAPOP=10 -YGAPORT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                       1 MOKSVPNKALELKNEQTLRA......SVRFLTLMKMKIISYMKIAC 398
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                              nucleic search, using frame_plus_p2n model
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Database :

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BP313026 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR01939, mRNA sequence.

BP313026.1 GI:52242001
1000 AGATGGTCTTCTGAAGCCTACCTGTGGAAGGAAGTTTCTCTTCCAAATAAAGCCTTAGA 2059
                                                                                                                             TIGGGATITIGAGGTITCCTIGAGGCTCTCTTACAGAATGATGGGTGTTTACCCAAGGC 2299
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                                   96 uLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGluPr 116
                                                                                                       116 oAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnTh 136
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1 (bases 1 to 581)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)
                                                                                                                                                                           rLeuArgAlaAspGlu1leLeuProSerGluSerLysGlnLysAspTyrGluGluSerSe
                                                                                                                                                                                                                                                                                                                      aThrHisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluGerProAspAsnAs
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                                                         216 uMetAspMetGlnThrPhetysAlaGluProProGluLysProSerAlaPheGluProAl
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                                                                                                                                                                                                                                                  rTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuProLysAl
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                                                                      Direct Submission
Submitted (13-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 46 Row: i Column: 20. This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORP
                                                                                                                                                                      Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shira
Toshiyuki and Plero Carninci (RIKEN)
TOShiyuki and Plero Carninci (RIKEN)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadam@systemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASDGlyLeuLeuLygAlaAsnCysGlyMetLysValSerIleProThrLysAlaLeuGl
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 Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone has the following problem: frame shifted.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3443
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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/mol_type="mRNA"
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/tissue type="Testis"
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us-09-489-079-24.rst

FEATURES

ORIGIN

Score:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (Bases I to 582)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizubhima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8619, Japan

Email: ysuzukidana.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuproSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeu 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheLysAlaGluProProGluLysProSerAlaPheGluProAlaIleGluMetGlnLys 122
                                                                                                                                                                                                                                                                1. .582
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/note="mammary gland tumor"
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DB:
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AUTHORS
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BP313436 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR03209, mENA sequence.
BP313436
BP313436.1 GI:52242411
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                                                                            1. :582

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                 Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yawawi@ims.u-tokyo.ac.jp.
Location/Qualifiers
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Conservative:
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    Department of Virology
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Best Local Similarity:
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Pred. No.:
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BP313704 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR03974, mRNA sequence.
121 GlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAsp 140
                   GluIleLeuProSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGlu 160
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                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 582)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizukihima-Sugano, J., Nakai, K. and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
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                                                                                                                                                                                    579
                                                                                                                                             161 SerLeuCysGluThrValSerGlnLysAspValCysLeuProLysAlaThrHisGln 179
                                                                                               463 GAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAAAGTTCTTGGGATTCTGAG
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Location/Qualifiers
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Mismatches:
Indels:
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Homo sapiens
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                                                                                     DP314867 Sugano cDNA library, mammary gland OCUB-F Homo sapiens CDNA clone OFR07276, mRNA sequence.
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Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Suzuki, Y., Yamashita, R. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol type="mRNA"
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/clone="058707276"
/tissue type="mammary gland"
/clone type="mammary gland"
/clone ill="Sugano cDNA library, mammary gland OCUB-F"
/note="mammary gland tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuaki@ims.u-tokyo.ac.jp.
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/db xref="texon:9606"
/dev stage="Adult"
/clone lib="BN0192"
/note="Organ: breast normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human.Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-BN0192-010900-025-E09&t3=2000-09-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence stop: 525.
High quality sequence stop: 525.
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                                             AAGGCTAACTGCGGAATGAAGTATCTATTCCAACTAAAGCCTTACAATTGATGGACATG 338
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RC5-BN0192-010900-025-E09 BN0192 Homo sapiens CDNA, mRNA sequence.
BF328582
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Fax: +55-11-2707001
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Bukaryogia.

Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 582)

Suzuki,Y.; Yamashita,R.; Shirota,M.; Sakakibara,Y.; Chiba,J.;

Mizushima-Sugano,J.; Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

Dontact: Yuteak Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo
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No. 196,716 - Ludwig Institute for Cancer Research) profiles into the DUC 18 vector. Reverse transcription tissue mRNA and cDNA amplification were performed under low stringency conditions."
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wx63g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2548376 3', mRNA sequence.
A1951118
A1951118.1 GI:5743428
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                                                                                                                                                                                                                  mammary gland OCUB-F"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 GluileAspLysileAsnGlyLysLeuGluGlySerProValLysAspGlyLeuLys
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                           582
160
10
0
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Matches:
Conservative:
Mismatches:
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Homo sapiens (human)
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Best Local Similarity:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 582)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mixushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
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                                                                                                                                                                                                                                                                                                                                                                                     102 GGGTCTCCTGTTAAAGAIGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 TCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAGGCCTTGGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATGAAGAAAGTTCTTGGGATTCTGAGAGTCTCTGTGGAGACTGTTTCACAGAAGGATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 ACTAAAGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAsp
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1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
1: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1. 582
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Matches:
Conservative:
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Best Local Similarity:
      4-6-1,
Email:
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Pred. No.:
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189 101 249

81

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369 161 429 181 489 549

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BP312910
BP312910 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR01441, mRNA sequence.
BP312910
BP312910.1 GI:52241885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 AgnGluGlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyr 152
     AspThrileHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnCys 338
                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 598)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Marushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="mammary gland"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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Mismatches:
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                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapber Strausberg, Ph.D.
Email: cgapber Tamail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2157 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 423.
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/lab host="DH10B"
/clone_lib="NCI_CGAP_Br18"
/clone_lib="NCI_CGAP_Br18"
/note="Organ: Dreast; Vector: pCWV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluSerLeuArgGluThrValSerGlnLy8AspValCy8ValProLy8AlaThrHisGln 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspGlnMetPheProSerGluSerLysGlnLysAsnValGluGluAsnSerTrpAspSer 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeuSerLysIleLeu 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnLysGlulleAspLysIleAsnGlyLysLesLuGluGluSerProAspAsnAspGlyPhe 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeuGluLeuMetAsp 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429 CTGAAGGCTCCCTGCAGAATGAAAGTTTCTATTCCAACTAAAAGCCTTAGAATTGATGGAC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGluProAlaIleGlu 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 AAAGAAATGGATAAAATAAGTGGAAAATTAGAAGATTCAACTAGCCTATCAAAAATCTTG 70
         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 490)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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/db_xref="taxon:9606"
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806.00
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EST 17-SEP-2004
                      TyrGluGluSerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspVal 171
                                                                                         CysLeuProLysAlaThrHisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGlu 191
                                                                                                                                                                                                                211
                                                                                                                                                                                                                                               462 ricricitaraagarigarcricigaaggcraacrigoggaarigaaggrircrarricaacr 521
                                                                                                                                                                                                                                                                                  LysalaLeuGluLeuMetAspMetGlnThrPheLysAlaGluProFroGluLysProSer 231
LysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAsp 151
                                                                                                                                                                            TGTTTACCCAAGGCTGCGCATCAAAAAGAAATAGATAAAATAAAATGAAATTAGAAGGG 461
                                                                                                                                                                                                                                                                                                                      522 AAAGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCATCT 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Justicy, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Makai, Y., Makai, K. and Sugano, S. Sequence comparizon of human and mouse genes reveals a homologous block structure in the promoter regions Genome Res. 14 (9), 1711-1718 (2004)

Genome Res. 14 (9), 1711-1718 (2004)

Department of Virology

Institute of Medical Science, University of Tokyo 10stitute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: Jocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 584)

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BP314652 Sugano cDNA library, mammary gland OCUB-F Homo sapiens
cDNA clone OFR06752, mENA sequence.
BP314652
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Mismatches:
Indels:
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757.00
89.08%
87.36%
36.89%
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                      BP315806 50 mRNA linear EST 17-SEP-2004 BP315806 Sugano cDNA library, mammary gland OCUB-F Homo sapiens CDNA clone OFR09418, mRNA sequence.
BP315806
                                                                                                      479
                    GAAGAAAGTTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTG 419
                                                                 173 LeuProLysAlaThrHisGlnLysGluIleAspLy8IleAsnGlyLysLeuGluGluSer 192
                                                                                                                                                             480 CCTGTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAA 539
 GluGluSerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCys 172
                                                                                                                                       193 ProAspAsnAspGlyPheLeuLysAlaProCysArgMetLysValSerileProThrLys 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 582)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91
                                                                                                                                                                                                            /tissue_type="mammary gland"
/cell_line="COUB-F"
/clone_lib="Sugano CDNA library, mammary gland OCUB-F"
/note="mammary gland tumor"
                                                                                           GlySerProValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIlePro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 ACTAAAGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerAlaPheGluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp.
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Matches:
Conservative:
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="0FR09418"
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95.62%
95.62%
38.06%
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BP315806
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GlySerProValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIlePro
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EST.
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Homo sapiens
Homo sapiens
Homo sapiens
Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Homo sapiens
Eukaryota; Matazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 583)
Suzuki,Y., Yamaabhita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Hofoli, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukidana.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                           BP313822 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR04566, mRNA sequence.
                                                                                                                                                238
                                                 132
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                                                                                                  152
                                                                                                                         358
                                                                                                                                                                                                LeuProLysAlaThrHisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSer 192
                                                                                                                                                                                                                                                   193 ProAspAsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLys 212
                                                                                                                                                                                                                         AlaPheGluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLys
                                                                    239 GCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAG
   LysalaLeuGluLeuMetAspMetGlnThrPheLysalaGluProProGluLysProSer
                AsnGluGlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyr
                                                                                                                        213 AlaLeuGluLeuMetAspMetGlnThrPheLysAlaGluPro 226
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OFR04566"
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BP313822.1 GI:52242797
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85.38%
84.21%
34.80%
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BP313822
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Bukaryota; Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi; Mammalia; Butboria; Primates; Catarrhini; Hominidae; Homo.

B. 1 (bases 1 to 582)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Contact: Yutachory in the promoter regions

Location Res. 14 (9), 1711-1718 (2004)

Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutachory

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzukielms. u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP313235 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR02569, mRNA sequence.
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71 GGGTCTCCTGTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAGTTTCTATTCCA 130
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/note="mammary gland tumor"
                                                                                                                                                                                                                                                                                                491 CTICIGATAGCIAACIGCGGAAIGAAGTIICIATICCAACTACTGCCTIAAAACTGATG
                                                      ThrLysAlaLeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysPro
                                                                                                           131 ACTAAAGCCTTAGAATTGATGGACATGCAAACTTTCAAAGCAGAGCCTCCCGAGAAGCCA
                                                                                                                                                               SeralaPheGluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeu
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Search completed: August
Job time : 15149.7 secs
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Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki

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Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers
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Mammalia; Butheria, Primates; Catarrhini, Hominidae, Homo.

    (bases 1 to 583)

                                                                                                            GlySerProValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIlePro
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                                                                                                                                      GGGCCTCCTGTTAAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAGTTTCTATTCCA
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460 AGATATGCTGCTGAATTTAGAACATTCTCTGCAATGATAAGGACTCCTGTTAAAGATGGT
Length:
Matches:
Conservative:
Mismatches:
Indels:
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/note="mammary gland tumor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BS322-specific polynucleotides, polypeptides and antibodies, used i
detection and diagnosis of breast disease especially breast cancer.
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                                                                                                                                                                                                                BS322; breast tissue marker; breast disease; breast cancer.
                                                                                                                                                           Amino acid sequence of BS322 polypeptide
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AAB07638 standard; protein; 398 AA
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Matches 398; Conservative
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Granados EN, Hodges SC,
Stroupe SD;
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                                                                                               QKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKATHQK 180
                                                                                                                                                                                            KSVPNKALELKNEQTLRADQMPPSESKQKNVEENSWDSESLRETVSGKDVCVPKATHQKE 300
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             1 MOKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAAHQ
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MQKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAAHQ
                                                                                                                                              EIDKINGKLEESPONDGFLKAPCRMKVSIPTKALELMDMQTFKARPPEKPSAFEPAIEMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the coding sequences and some protein sequences of proteins associated with breast cancer in humans. These sequences can be used in the diagnosis and treatment of cancers, particularly breast tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An isolated polypeptide useful for the treatment and diagnosis of e.g. breast cancer comprises at least an immunogenic portion of a tumor protein.
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99US-00339338.
99US-00389681.
99US-00433826.
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23-JUN-1999;
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03-NOV-1999;
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                                                                                                                             QKSVPNKALELKNEQTLRADEILPSESKQXDYEESSWDSESLCETVSQXDVCLPKATHQK 180
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                                                                                                                                                                                                                                                                      Genetic subtraction; DNA microarray analysis; polymerase chain reaction; cancer; B726P.
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                                                       253 MQKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAXHQ
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Length 650,
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 Score 2023; DB 4;
Pred. No. 7.1e-150;
1; Mismatches 4;
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20-UUL-2000; 2000US-0219662P.
27-UUL-2000; 2000US-021300P.
18-DEC-2000; 2000US-0256592P.
  Query Match 98.6%;
Best Local Similarity 98.7%;
Matches 393; Conservative
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522
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N-PSDB; AAI67218.
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20-JUL-2000;
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Identifying tissue (tumor)-specific polynucleotides overexpressed in tissue of interest as compared to control tissue, for detecting cancer cells in patient, comprises DNA microarray analysis or quantitative
                                                      Example; Page 108-111; 127pp; English
                                   polymerase chain reaction.
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The invention relates to identifying tissue-specific polynucleotides (P) from that involves performing a genetic subtraction to identify pool of from tissue of interest (TI), performing DNA microarray analysis to identify first subset of polynucleotides (SP1) at least 2-fold over expressed in TI, and performing quantitative polymerase chain reaction (PCR) analysis on SP1 to identify second subset of (P). The method is useful for determining the presence or absence of a cancer cell in patient, monitoring the progression of cancer in a patient using a biological sample such as blood, serum, lymph nodes, bone marrow, sputum, urine or a tumour biopsy sample. The methods are useful for determining the presence of or monitoring progression of prostate, breast, ollon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver, gastric, kidney, bladder, pancreatic or endometrial cancer. Sequences ARG65983-987 represent determined splice variants of B726P

Sequence 650 AA;

372 180 432 240 492 300 552 360 612 KEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEM 120 9 KEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEM MDKISGKLEDSTSLSKILDTIHSCERARELQKDHCEQCTGKMEQMKKKFCVLKKKLSEAK MQKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAXHQ QKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKATHQK **OKSVPNKALELKNE** OTLRADEIL PSESKOKDYBESSWDSESLCETVSOKDVCL PKAXHOK BIDKINGKLESPDNDGFLKAPCRMKVSIPTKALBLMDMGTFKAEPPEKPSAFEPAIEMQ KSVPNKALELKNEQTLRADQMFPSESKQKNVEENSWDSESLRETVSQKDVCVPKATHQKE KSVPNKALELKNEQTLRADQMPPSESKQKXVBENSWDSESLRETVSQKDVCVPKATHQKE 1 MOKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAAHQ Gaps ö 98.6%; Score 2023; DB 4; Length 650; 98.7%; Pred. No. 7.1e-150; Indels EIKSQLENQKVKWEQELCSVRFLTLMKMKIISYMKIAC 398 1; Mismatches Matches 393; Conservative Best Local Similarity 313 373 553 61 121 181 433 241 493 301 361 Query Match g g g g 셤 ઠે 8 ઠે ò 셤 ઠે ઠે

AAU33346; RESULT 4 AAU33346

AAU33346 standard; protein; 650 18-DEC-2001 (first entry)

Human breast cancer protein encoded by cDNA B726P-spliced seq_B726P. ss; breast cancer protein; tumour; cancer; cytostatic; gene therapy; immunogen. Human;

Homo sapiens

The invention relates to isotated press to under processing and incircing and antibodies that encode them, including immunogenic fragments of the proteins.

Also included are expression vectors expressing the proteins, transformed cells and antibodies raised against the proteins or an antigen presenting cell expressing the protein. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with the prevention, diagnosis and expression, i.e. breast tumours and breast cancer e.g by gene therapy. The nucleic acids and their complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The proteins may be used in assays to identify modulators (e.g. antagonists) of breast tumour protein expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down capulate approach and activity. The antibodies may also be used to down capulate approach and activity are presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immunopur protein encoded by a cDNA fibrart cumour protein encoded by a cDNA fibrart a normal breast cDNA QKSVPNKALELKNEQTLRADEILPSESKOKDYEESSWDSESLCETVSOKDVCLPKATHQK 180 313 KEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEM **EIDKINGKLEESPDNDGFLKAPCRMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEMQ** KEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEM KSVPNKALELKNEQTLRADOMPPSESKOKNVEENSWDSESLRETVSOKDVCVPKATHOKE MQKSVPNKALELKNEQTLRADE1LPSESKQKDYEESSWDSESLCETVSQKDVCLPKAAHQ Gaps The invention relates to isolated breast tumour proteins and nucleic Hepler WT; Breast Tumor Proteins and nucleic acids useful for the prevention diagnosis and treatment of breast cancer. ö 4; Indels Harlocker SL, Score 2023; DB 4; Pred. No. 7.1e-150; 1; Mismatches 4; Χu J, Claim 3; Page 275-276; 297pp; English Mitcham JL, 98.6**%**; 98.7**%**; 17-APR-2000; 2000US-00551621. 08-JUN-2000; 2000US-00590751. 22-JUN-2000; 2000US-00604287. 20-JUL-2000; 2000US-0062040S. 12-APR-2001; 2001WO-US012164 Matches 393; Conservative Jiang Y, Dillon DC, (CORI-) CORIXA CORP. WPI; 2001-611721/70. N-PSDB; AAS47405. Similarity Sequence 650 AA; WO200179286-A2 25-OCT-2001 433 241 61 121 181 493 Query Match Best Local 셤 셤 8. S Š ð Š ઠે

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432 240 492 300 552

MDKISGKLEDSTSLSKILDTIHSCERARELQKDHCEQCTGKMEQMKKKFCVLKKKLSEAK 360

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MDKISGKLEDSTSLSKILDTVHSCERARELQKDHCEQRTGKMEQMKKKFCVLKKKLSEAK 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel breast cancer polynucleotides and polypeptides encoded by the polynucleotides, useful for detecting the presence of breast cancer in a patient, and in pharmaceutical compositions, for treating breast cancer.
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                                                                                                                                                                                                              Human; breast tumour protein; breast cancer; cytostatic; vaccine.
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larity 98.7%; Pred. No. 7.1e-150;
Conservative 1; Mismatches 4; Indels
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                                       EIKSQLENQKVKWEQELCSVRFLTLMKMKIISYMKIAC 398
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                                                                                                                                                                                     Human breast tumour polypeptide #5
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                                                                                                             ABG78913 standard; protein; 650
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990S-0039338
990S-0039338
2000US-00551621
2000US-0055051751
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N-PSDB; ABS64006.
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08-JUN-2000;
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373 QKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAXHQK 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fanger GR;
313 KEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKALELMUMQTFKAEPPEKPSAFEPAIEM
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                                                  OKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKATHQK
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Henderson RA,
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Xu J, Harlocker SL, Hepler WT,
Mcneill PD, Durham M;
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07-DEC-2001; 2001US-00007805.
13-FEB-2002; 2002US-00076622.
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Vedvick TS,
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1 MOKSVPNKALELKNEQTLRADEILPSESKOKDYBESSWDSESLCETVSOKDVCLPKAAHQ

Local Similarity nes 393; Conserv

Best Loca Matches

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us-09-489-079-24.rag

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Human breast cancer
N-PSDB; ADL93125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell expander
                                                                                                        Sequence 650 AA;
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02-APR-1999;
23-JUN-1999;
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                                                                                                                     Query Match
Best Local S
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                                                                                   313 KEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEM 372
                                                                                                        121 QKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKATHQK 180
                                                                                                                                                     492
                                                                                                                                                                                                   MDKISGKLEDSTSLSKILDTIHSCERARELQKDHCEQCTGKMEQMKKKFCVLKKKLSEAK 360
                                                                                                                                       EIDKINGKLEESPDNDGFLKAPCRMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEMQ
                                                                                                                                                                               1 MOKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAAHQ
                                                                                                                                                                                                                                                                                                                                                   cancer; human.
                               Gape
                               ö
                Length 650;
                               Indels
                                                                                                                                                                                                                                                                                                                                                   gene therapy; protein therapy; vaccine; breast cancer;
                                                                                                                                                                                                                                  EIKSQLENOKVKWEQELCSVRFLTLMKMKIISYMKIAC 398
                                                                                                                                                                                                                                          Score 2023; DB 6;
Pred. No. 7.1e-150;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                     Human breast cancer-associated polypeptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Persing DH;
                                                                                                                                                                                                                                                                                        ADL93131 standard; protein; 650 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-1998; 98US-0022575.
02-APR-1999; 99US-00285480.
22-JUN-1999; 99US-00339338.
02-SEP-1999; 99US-00338261.
03-NOV-1999; 99US-00433826.
17-APR-2000; 2000US-00551621.
22-JUN-2000; 2000US-005604287.
20-JUL-2000; 2000US-006604287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-APR-2001; 2001US-00834759
07-DEC-2001; 2001US-00007805
13-FEB-2002; 2002US-00076222
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                98.6%;
98.7%;
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                               Conservative
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                        Similarity
  Seguence 650 AA
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              Query Match
Best Local Simi
Matches 393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612
                                                                                                            The invention relates to an isolated breast cancer-associated polypeptide. The polypeptide may be used for the diagnosis and treatment of breast cancers. The methods are useful for detecting the presence of a cancer in a patient and treating a cancer in a patient. The present sequence represents the amino acid sequence of a human breast cancerassociated polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                              9
    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 MQKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAXHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             493 KSVPNKALELKNEGTLRADQMFPSESKQKKVEENSWDSESLRETVSQKDVCVPKATHQKE
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                                                                                                                                                                                                                                                                                                                                                                               Gaps
An isolated oncogenic polypeptide useful for preventing, diagnosing treating breast cancer.
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                                                                                                                                                                                                                                                                                                                                Length 650;
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                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIKSQLENOKVKWEQELCSVRFLTLMKMKIISYMKIAC 398
                                                                                                                                                                                                                                                                                                                                98.6%; Score 2023; DB 7;
98.7%; Pred. No. 7.1e-150;
cive 1; Mismatches 4;
                                                                       Example 1; SEQ ID NO 469; 294pp; English
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99US-00285480.
99US-00339338.
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                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 98.7
Matches 393, Conservative
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cancer protein; tumour; cancer; cytostatic;

(first entry)

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Human breast cancer protein B726P fusion protein #2.
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08-UTN-2000; 2000US-005951.
22-UTN-2000; 2000US-0064287.
20-UTL-2000; 2000US-006204057.
                                                                                                                                                                                                                                                                                12-APR-2001; 2001WO-US012164.
                                                                                                                   Human; ss; breast cance:
gene therapy; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                        Jiang Y, Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-611721/70
                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP
                                                                                                                                                                                                            WO200179286-A2.
                                                                                                                                                                            Homo sapiens
                                                 18-DEC-2001
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                AAU33358;
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                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polypeptide comprising at least an immunogenic portion of a breast tumour protein. The polymucleotide, its polypeptide, its antibody, a pharmaceutical composition comprising the fusion protein or the polymucleotide encoding it, a vaccine comprising the fusion protein or the polymucleotide encoding it, an isolated T cell to population comprising T cells specific for a breast tumour protein, and a method for removing tumour cells from a biological sample is useful for inhibiting the development of a cancer in a patient. The polypeptide is useful for expanding T cells specific for a breast tumour protein is useful for inhibiting the development of a cancer in a patient. The method additionally involves the step of cloning at least one proliferated cell and then administering the cloned T cells at least one proliferated cell and then administering the cloned T cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKATHQK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSVPNKALELKNEQTLRADQMFPSESKQKNVEENSWDSESLRETVSQKDVCVPKATHQKE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                             Novel isolated polypeptide comprising immunogenic portion of breast tun protein or its variant, useful for formulating vaccines for inhibiting cancer development in a patient.
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                                                                                                                                                          Harlocker SL
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                                                                                                                                                          Χu J,
                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 469; 217pp; English
                                                                                                                                                          Mitcham JL,
99US-00389681.
99US-00433826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                       HARLOCKER S L.
                                                                                                                                                        Jiang Y, Dillon DC,
                                                                                    MITCHAM J L.
                                                                                                                                                                                           WPI; 2004-020270/02
                                                   JIANG Y.
DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
1es 393; Conserv
                                                                                                                                                                                                            N-PSDB; ADE44415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 650 AA;
02-SEP-1999;
03-NOV-1999;
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                                                                                  (MITC/)
(XUJJ/)
(HARL/)
                                                   (JIAN/)
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Matches
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Hepler WT;

Harlocker SL,

Xu J,

Mitcham JL,

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                                                                                                                                                                                                                                                       The invention relates to isolated breast tumour proteins and nucleic acids that encode them, including immunogenic fragments of the proteins. Also included are expression vectors expressing the proteins, transformed cells and antibodies raised against the proteins or an antigen presenting cell expressing the protein. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate breast tumour protein expression, i.e. breast tumours and breast cancer e.g by gene therapy. The nucleic acids and their complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The proteins, nucleic acids and antibodies may be used in assays to identify proteins, nucleic acids and antibodies may be used in assays to identify
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modulators (e.g. antagonists) of breast tumour protein expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immunotaristic adjance to techniques. The present sequence is a breast tumour protein encoded by a CDNA from a breast tumour cDNA library isolated by subtractive hybridisation against a normal breast CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MQKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAAHQ
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                                                                   Breast Tumor Proteins and nucleic acids useful for the prevention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2023; DB 4;
Pred. No. 8.6e-150;
1; Mismatches 4;
                                                                                                                 diagnosis and treatment of breast cancer.
                                                                                                                                                                                             Claim 23; Page 295-296; 297pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.6%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 393; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
N-PSDB; AAS47422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 743 AA;
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AAU33358 standard; protein; 743 AA

RESULT 9
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tumour polypeptide of the invention
                                                                   Sequence 743 AA;
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                                                                                                                                                                                                                                        MDKISGKLEDSTSLSKILDTIHSCERARELQKDHCEQCTGKMEQMKKKFCVLKKKLSEAK 360
                                                                                                                                                                                                                                                                                                                                                                    546 MDKISGKLEDSTSLSKILDTVHSCERARELQKDHCEQRTGKMKKRFCVLKKKLSEAK 705
                                                                                                                                                                                               KSVPNKALELKNEQTLRADQMFPSESKQKNVEENSWDSESLRETVSQKDVCVPKATHQKE 300
      QKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAXHQK 525
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                                                                                                        BIDKINGKLEESPDNDGFLKAPCRMKVSIPTKALELMDMQTFKAEPPEKFSAFBAIEMQ
                                                                      EIDKINGKLEESPDNDGFLKAPCRMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIKSQLENQKVKWEQELCSVRFLTLMKMKIISYMKIAC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIKSQLENQKVKWEQELCSVRFLTLMKWKIISYMKIAC 743
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990S-00285480.
990S-003938.
990S-00389681.
990S-0043826.
2000US-00551621.
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20-JUL-2000; 2000US-00620405
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Henderson RA;
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17-APR-2000;
08-JUN-2000;
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23-JUN-1999;
02-SEP-1999;
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                                                                            1 MOKSVPNKALELKNEQTLRADBILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAAHQ
                                                                                                                      346 MQKSVPNKALELKNEQTLRADBILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAXHQ
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; vaccine; gene therapy; T cell stimulation; T cell expansion; tumour; breast cancer; cancer; immune response stimulation.
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Henderson RA,
    Length 743
                                       4; Indels
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  Score 2023; DB 5;
Pred. No. 8.6e-150;
1; Mismatches 4;
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tu J, Harlocker SL, Hepler WT,
Icneill PD, Durham M;
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07-DEC-2001; 2001US-00007805.
13-FEB-2002; 2002US-00076622.
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    98.6%;
98.7%;
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Query Match
Best Local Similarity 98.7
Matches 393; Conservative
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Vedvick TS,
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08-JUN-2000; 2000US-00590751.
22-JUN-2000; 2000US-00604287.
20-JUL-2000; 2000US-00620405.
13-ARR-2001; 2001US-00834759.
07-DEC-2001; 2001US-00007805.
13-FEB-2002; 2002US-00076622.
                                                                                                                                                                                                                                                        associated polypeptide.
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                                                                          CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                              Sequence 743 AA;
                                                                                              Houghton RL,
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                                 cella
                                          specific for a tumour protein. The invention further comprises human nucleic acids and proteins that are associated with tumours (e.g. breast
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                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
                                                             cancer). The method and sequences of the invention are useful for stimulating and/or expanding T cells specific for a tumour protein, detecting the presence of cancer, stimulating an immune response in patient and treating breast cancer. The present amino acid sequence represents a human tumour-related protein
                                invention comprises a method of stimulating and/or expanding T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein therapy; vaccine; breast cancer; cancer;
                                                                                                                                                 98.6%; Score 2023; DB 6; Length 743; 98.7%; Pred. No. 8.6e-150; ive 1; Mismatches 4; Indels
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           Disclosure; Page 312-314; 375pp; English
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99US-00285480.
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99US-00438681.
99US-00433826.
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Best Local Similarity 98.7
Matches 393, Conservative
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                                                                                                                            Sequence 743 AA;
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02-APR-1999;
23-JUN-1999;
02-SEP-1999;
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17-APR-2000;
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                                                                                                                                                                                                                                                                                                                        polypeptide. The polypeptide may be used for the diagnosis and treatment of breast cancers. The methods are useful for detecting the presence of cancer in a patient and treating a cancer in a patient. The present sequence represents the amino acid sequence of a human breast cancer-
                                                                                                                                              isolated oncogenic polypeptide useful for preventing, diagnosing and
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                                                                                                                                                                                                                                                                                                The invention relates to an isolated breast cancer-associated
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Pred. No. 8.6e-150;
1; Mismatches 4;
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                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 494; 294pp; English
   HO.
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   Persing
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Best Local Similarity 98.7%;
Matches 393; Conservative
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Sleath PR,
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ADL93214 standard; protein; 661
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                                                                                                                                                            Fanger
                                                                                                                                                                                                                                                                     The invention comprises a method of stimulating and/or expanding T or specific for a tumour protein. The invention further comprises human nucleic acids and proteins that are associated with tumours (e.g. brocancer). The method and sequences of the invention are useful for stimulating and/or expanding T cells specific for a tumour protein, detecting the presence of cancer, stimulating an immune response in spatient and treating breast cancer. The present amino acid sequence represents a human tumour-related protein
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                           New polypeptide and polynucleotide useful for stimulating and/or expanding T cells specific for a tumor protein and treating breast
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                                                                                                                                                  Persing DH, Jiang Y, Dillon DC;
ker SL, Hepler WT, Henderson RA,
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Pred. No. 1.8e-149;
4; Mismatches 3;
                                                                                                                                                                                                                                                     Example 8; Page 332-334; 375pp; English
                                                                                                                                                  Sleath PR, Persing DI
Xu J, Harlocker SL, I
Mcneill PD, Durham M;
                                                                                                                                                                                                                                                                                                                                                                                     98.3%;
98.2%;
                                                                                      13-APR-2001; 2001US-00834759.
07-DEC-2001; 2001US-00007805.
13-FEB-2002; 2002US-00076622.
                                                                      15-APR-2002; 2002WO-US012378
                                                                                                                                                                                                                                                                                                                                                                                                      Matches 391; Conservative
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                                                                                                                                                                                        WPI; 2003-103376/09.
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                               WO200283956-A1
                                                                                                                                                    Houghton RL,
            ношо варіепв
                                                  24-OCT-2002
                                                                                                                                                              Mitcham JL,
Vedvick TS,
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                                   gene therapy; protein therapy; vaccine; breast cancer; cancer; human.
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Human breast cancer-associated polypeptide #47
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2000US-00604287.
2000US-0063405.
2001US-00834759.
2001US-00007805.
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99US-00285480.
99US-00339338.
99US-004338261.
99US-00433826.
2000US-00551621.
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17-APR-2000;
08-JUN-2000;
22-JUN-2000;
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13-FEB-2002;
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                                                                                Homo sapiens
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14 RESULT 14 ADL93214

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The invention relates to isolated breast tumour proteins and nucleic acids that encode them, including immunogenic fragments of the proteins. The included are expression vectors expressing the proteins, transformed cells and antibodies raised against the proteins or an antigen presenting cell expressing the protein. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate breast tumour protein expression, i.e. breast tumours and breast cancer e.g by gene therapy. The nucleic acids and their complements may also be used as DNA probes in 'diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The conductors (e.g. antagonists) of breast tumour protein expression and activity. The antibodies and antagonists may also be used as sectivity. The antibodies and antagonists may also be used to down activity. The antibodies and antagonists may also be used as sectivity activity and cativity. The antibodies mad antagonists may also be used as sectivity activity also and activity. The antibodies may also be used as used as ciagnostic agents for detecting the presence of the protein in samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immunocided by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protein encoded by a cDNA from a breast tumour protei
564 MDKISGKLEDSTSLSKILDTVHSCERARELQKDHCEQRTGKMEQMKKKPCVLKKKLSEAK 623
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                                                                                                                                                                        361 BIKSOLENOKVKWEQELCSVRFLTLMKMKIISYMKIAC 398
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                                                                                                                                                                                                                                                                                                                                         AAU33351 standard; protein; 1002 AA.
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08-JUN-2000; 2000US-0059051.
22-JUN-2000; 2000US-00604287.
20-JUL-2000; 2000US-00620405.
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Sequence 1002 AA

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                                                                                253 MQKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAXHQ 312
                                                                                                                              61 KEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEM 120
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                                                                                                                                              313 KEIDKINGKLEGSPVKOGLLKANCGMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEM
                                                                                                                                                                                                              373 QKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAXHQK
                                                                                                                                                                                                                                                                                                                                          121 QKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKATHQK
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                                                              MQKSVPNKALELKNEQTLRADE1LPSESKQKDYEESSWDSESLCETVSQKDVCLPKAAHQ
                               Gaps
                               1,
Length 1002;
                               4; Indels
Score 1940.5; DB 4
Pred. No. 3.8e-143;
1; Mismatches 4;
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Query Match
Best Local Similarity 98.4%;
Matches 379; Conservative
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us-09-489-079-24.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 1, 2005, 22:08:06; Search time 24.5213 Seconds (without alignments) 1561.672 Million cell updates/sec

2052 1 MQKSVPNKALELKNEQTLRA.....SVRFLTLMKMKIISYMKIAC 398 US-09-489-079-24 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	kinesin-related pr		al	involucrin - human	centromere protein	protein H05009.1 [hypothetical prote			synaptonemal compl	microtubule bindin	probable myosin he	myosin heavy chain	ardiac	heavy	1pha	pole	myosin heavy chain	tical	₹	tin -	heavy	myosin heavy chain		smooth muscle myos	microtubule-vesicl	- huma	myosin alpha heavy	hypothetical prote
CHARAMAC	ΩI		T34418	F96673	A24168	S28261	E89066	T33247	832763	T51505	S49461	T13030	F84730	A26655	I49464	T18278	A46762	826710	A24922	T21174	138055	T14867	148175	804090	JC5421	JC5420	A43336	S22695	806005	T22976
	DB	7	~	7	н	Н	~	N	~	7	~	7	7	N	7	7	-	7	-	~	7	~	~	-	~	~	~	~	Н	0
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d	Query Match		8.9	8.7	8.4	8.4		8.5	8.2	8.1	8.0	8.0		7.9		7.9	7.9	7.9	7.9	7.9	7.8			7.7	7.7		7.6	7.6	7.6	7.6
	Score	182.5	182	179.5	173	171.5	169	169	168	165.5	164.5	164.5	163	163	162.5	162.5	162	161.5	161.5	161.5	161	158.5	158.5	158.5	158	158	156.5	156.5	156.5	156
	Result No.	-	7	٣	4	Ŋ	φ	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

105 AEPPE--KPSAFEPAIEMQKSVPNKALELKNEQTLRADEILPSESKOKDYEESSWDSESL 162

셤 ò 8 6 8 6 8

163 CETVSQKDVCLPKATHQKE-----FLKA 201

202 PCR------MKVSIPTKALELMDMQTFKAEPPE-----KPSAFEPAIEMQKSVPN 245

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Š 음 &

246 KALELKNEOTLRADQMFPSESKOKNVEENSWDSESLRETVSQKDVCVPKATHQKE--MDK 303

347 -KKFCVLKKKLSEAKE----IKSQLENQKVKWEQELCSVRFLTLMKMKIISYMK 395

304 ISGKLEDSTSLSKILDTIHSCERARELQKDHC--EQCTGKME----QMK----- 346

embryonic protein ribosome receptor,	nestin - golden ha 364K Golgi complex	involucrin L - gor coiled coil protei	transport protein	hypothetical prote	nonmuscle myosin i	protein UNC-89 - C	hypothetical prote	CG1 protein - huma	myosin heavy chain	hypothetical prote	surface membrane p	conserved hypothet
S39475 A56734	T34518 JC5837	I37060 T38435	867593	T24806	A59282	T29757	A86188	153799	T18296	T25410	PC6003	A70387
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474	1804	635	1790	1164	1964	6642	841	1300	2139	2331	624	978
7.6	7.6	7.5	7.5	7.5	7.5	7.5	7.4	7.4	7.4	7.4	7.4	7.4
155.5	155.5	154.5	154	153.5	153.5	153.5	152.5	152.5	152.5	152.5	152	152
30	333	34	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1
	T14156
	kinesin-related protein - African clawed frog
	C;Species: Xenopus laevis (African clawed frog)
	C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Ju1-2004
	C;Accession: T14156
	R; Wood, K.W.; Sakowicz, R.; Goldstein, L.S.; Cleveland, D.W.
	Cell 91, 357-366, 1997
_	A;Title: CENP-E is a plus end-directed kinetochore motor required for metaphase chromoson
	A; Reference number: Z17893; MUID: 98028574; PMID: 9363944
	A;Accession: T14156
_	A;Status: preliminary; translated from GB/EMBL/DDBJ
	A:Molecule type: mRNA
_	A;Residues: 1-2954 <woo></woo>
	A,Cross-references: UNIPROT:042263; EMBL:AF027728; NID:92586070; PID:92586071; PIDN:AAC60
	C;Genetics:
	A;Gene: XCENP-E
	C; Superfamily: centromere protein B; kinesin motor domain homology
	Query Match 8.9%; Score 182.5; DB 2; Length 2954;
	Š
	Matches 107; Conservative 83; Mismacches 1/1; indels 113; Gaps 21;
	QY 11 ELKNEQ-TLRADEILPSESKQKDYBESSWDSESLCETVSQKDVCLPKAAHQKEIDKIN 67
	Db 1792 ELKNSQRTVIAERDQLQDDLRESVEMSIETQDDLRKAQEALQQQKDKVQEL 1842
	Qy 68GKIRGSPVKDGLLKANCGMKVSIPTKALELMDMQTFK 104
	DD 1843 TSQISVLQEKISLLENQMLYNVATVKETLSERDDLNQSKQHLFSEIETLSLSLKEKE-FA 1901
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involucrin - human
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A;Gene: F13011.30
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C.Accession: F96673
F.Theologis, A. Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Con, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Alauthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | : | : | | : | | 307 EKLKIEAEANIKKTAEVEAAKKOKEKDEOLKLETEVVSKKSAAEKLELEKOAOIKKAAEA 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 KAEPPEKPSAFEPAIEMQKS---VPNKALELKNEQTL--RADEILPSESKQKDYEESSWD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            628 EQQPSDKNKSEVVGVPEKAAGPETKKDVSEIEEVPKKKTIKKKTEKSDSSISQKSNVLKP 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WDSESL-----RETVSQKDVCVPKATHQKEMDKISGKLEDSTSLSKILD 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 KEIDK------INGKLEGSPVKDGLLKANCGMKVSIPTKALELMDMQTF 103
                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Realdudes: 1-3488 <FUL>
A;Crosa-references: EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023; CESP:F12F3.3
A;Experimental source: strain Bristol N2; clone F12F3
                                                                                                                 hypothetical protein F12F3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 OKSVPNKALELKNEQTLRADEILPSESKOKDYEESSWDSESLCETVSOKDVCLPKAAH-Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MQTFKAEPPEKPSAFEPAIEMQ-KSVPNKALELKNEQT--LRADQMFPSESKQKNVEENS
                        2241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58; Gaps
2189 VKEVDELLQHLSSLKEQLDQIQMELRNEKLR-NYELCEKMDIMEKEISVLRLMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.9%; Score 182; DB 2; Length 3488; Best Local Similarity 23.7%; Pred. No. 0.034; Matches 106; Conservative 66; Mismatches 218; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1
                                                                                                                                                                                                               Rirulton, B.; Wohldmann, P. submitted to the EMBL Data Library, July 1998 A; Description: The sequence of C. elegans cosmid F12F3. A; Accession: T34418
                                                                                                                                                                                                                                                                                                                            Status: preliminary; translated from GB/EMBL/DDBJ
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H.; Tallon, I
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C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Rcference number: A86141; MUID:21016719; PMID:11130712
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1313 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 263, 18093-18098, 1988
A,Title: The glutamine residues reactive in transglutaminase-catalyzed cross-linking of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P07476; GB:M13902; GB:M13903; NID:g186519; PIDN:AAA59186.1; R;Simon, M.; Green, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 KDHCEQCTGKWEQMKKKFCVLKKKLSEAKEIKSQL-----ENQKVKWEQELCS 379
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C;Date: 25-Oct-1987 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: A24168
R;Eckert, R.L.; Green, H.
Cell 46, 583-589, 1986
A;Title: Structure and evolution of the human involucrin gene.
A;Reference number: A24168; MUD:86272107; PMID:2873896
A;Accession: A24168
A;Accession: A24168
A;Accession: A24168
A;Accession: A24168
A;Accession: A24168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MQKSVPNKALELKNB----QTLRADE--ILPSESKQKDYEESSWDSESLCETVSQKDVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 LELMDMQTFKAEP---PEKPSAPEPAIEMOKSVPNKALELKNEQTLR-----ADEILPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.7%; Score 179.5; DB 2; Length 1
22.9%; Pred. No. 0.015;
tive 91; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEDSTSLSKILDTIHSCE------
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1030 ORIEELTNLKOTLI 1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 22.9
Matches 113; Conservative
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Query Match
Best Local Similarity 21.4
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: H05009.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269
                                                                                                                                                                                                                                                                                                                                                                                                 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374
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                                                                 er modifications in vivo, allows modification at a number of other sites
CjComment: During the terminal differentiation of keratinocytes, this protein from the d
linked envelope under the plasma membrane.
CjGenetics:
AjGene: GDB:1U1
AjGene: GDB:1U1
AjGene: GDB:1U355; OMIM:147360
AjMap position: 1421-1421
CjSuperfamily: involucrin
CjSuperfamily: involucrin
CjSuperfamily: involucrin
FjS3-541/Region: 10-residue repeats (Q-E-G-Q-[PLV]-[KE]-[LH]-[PL]-E-Q)
Fj496/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of other proteins) #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :Cross-references: UNIPROT:Q02224; EMBL:Z15005; NID:G29864; PIDN:CAA78727.1; PID:G2986
                 or intact and fragme exclusive preferend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: centromere protein B; kinesin motor domain homology
C;Keywords: ATP; coiled coil; microtubule binding; mitosis; nucleotide binding; P-loop
F;7-35;Domain: kinesin motor domain homology «KMOT»
F;86-93;Region: nucleotide-binding motif A (P-loop)
F;486-2183;Domain: coiled coil #status predicted «COI»
                 A; Contents: annotation; transglutaminase-catalyzed cross-link sites of intact and fragm A;Note: in vitro studies of native, soluble involucrin showed almost exclusive preferer er modifications in vivo, allows modification at a number of other sites C; Comment: During the terminal differentiation of keratinocytes, this protein from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N'Alternate procession contromere 312K protein; kinesin-related protein CENP-E
N'Alternate names: centromere 312K protein; kinesin-related protein CENP-E
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S28261
R;Yen, T.J.; Li, G.; Schaar, B.T.; Szilak, I.; Cleveland, D.W.
Nature 359, 536-539, 1992
A;Tile: CENP-E is a putative kinetochore motor that accumulates just before mitosis. A;Reference number: S28261; MUID:93024922; PMID:1406971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPEQQLKQEKTQRDQQLNKQLEEEKKLLDQQLDQELVKRDEQLGMKKEQLLELPEQQE-- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPKAAHQKEIDKINGKLEGSPVKDGLLKANCGMKVSIPTK---ALELMDMQTFKAEPPEK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSAFEPAIEMQKSVPNK---ALELKNEQTLRADEILPSESKQKDYEESSWDSESLCETVS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0-----EGQLELPEQOEGQLELPQQQ----EGQLELSEQQEGQLELSE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 ÓQEGQLICHLEHÓE-----GQLEVPEEQMGQLK----YLEQQEGQLKHLDQQEKQPELP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKPSAFEPAIEMQKSVPNKALELKNEQTLRADQMFPSESKQKNVEENSWDSESLRETVSQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 KDVCVPKATHQKEMDKISGK---LEDSTSLSKILDTIHSCERARELQKDHCEQCTGKMEQ 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 IGLPEQQVLQLKQLEKQQGQPKHLEEEEGQLK----HLVQQEGQLK--HLVQQEGQLEQ 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 NKALELKNEQTLRADEI---LPSESKQKDY------EESSWDSESLCETVSQKDVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QXDVCLPKATHQKE1DK1NGKLESPDNDGFLKAPCRMKVS1PTKALELMDMQTFKAEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 EQQMGQLKHLEQQEGQP-KHLE---QQEGQLEQLEEQEGQLKHLEQQEGQLEHLEHQEGQ
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    70;
                                                                                                                                                                                                                                                                                                                                                8.4%; Score 173; DB 1; Length 585; 23.5%; Pred. No. 0.014; ive 70; Mismatches 160; Indels
Reference number: A57786; MUID:89053976; PMID:2461365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 MKKKFCVLKKKLSEAKEIKSQLENQKVKWEQE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: GDB:361164; OMIM:117143
A, Map position: 4q24-4q25
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 23.5
Matches 92; Conservative
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A;Molecule type: mRNA
A;Residues: 1-2663 <YEN>
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procesin H05009.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E89066
R;anonymous, The C: elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C: elegans: a platform for investigating biology
A;Title: Genome sequence of the nematode C: elegans; and www sanger.ac.uk/Projects/C elegans h)Note: see websites genome.wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
A;Notesidues: 1-2109 <STO>-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1070 KTDLKENIEMTIENQESLKLLGDELKKQQEIVAQEKNH------AIKKEGE 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1115 LSRTCDRLAEVERTIKEKSQQLQEKQQQLLANVQEBMSEMQKKINBIENLKNBLKNBLFUTL 1174
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                                                            24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KNVEENSWDSESLR----ETVSQKDVCVPKATHQKEMDKISGKLEDSTSLSKILD 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 AHOKEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKALELMDMQTFKAEPPEKPSAFEPA 117
                                                                                                                                                                                                                                          55 PKAAHQKEIDKINGKLEG-SPVKDGLLKANCGMKVSIPTKALELMDMQTFKAEPPEKPSA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIHSCERARELQ----KDHCEQCTGKMEQM---KKKFCVLKKKLSEAKEIKSQLENQKVKW 373
                                                                                                                                                                                                                                                                                                                                                                                                    782 SEVVHKE--SRVQGLLEEIGKTKDDLATTQSNYKSTD-----QEFQNFKTLHMDFEQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------OMFPS---ESKO-
                                                                                                                        1 MOKSVPNKALBLKNEQTLRADEILPSESKOKDYE-----ESSWDSESLCETVSOKDVCL
                                                                                                                                                                                 725 LOKEL-NK--EVEENEALREEVILLSELKSLPSEVERLRKEIQDKSEELHIITSEKDKLF
                                                                                                                                                                                                                                                                                                                                                                     114 FEPAIE----MQKSVPNKALE-----LKNEQTLRADEILPSESKQKDYEESSWDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESLCETVSQKDVCLPKATHQKEI--DKINGKLEE----SPDNDGF-----LK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 APCR--MKVSIPTK----ALELM-----DMQTFKAEPPEKPS-----AFEPAIEMQ
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                                                        84; Mismatches 157; Indels 137;
Length 2663;
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rive 77; Mismatches 173;
   DB 1;
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   Score 171.5; DB
Pred. No. 0.095;
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23.1%; Pred. No. 0.1;
      8.4%;
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us-09-489-079-24.rpr

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C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S32763; I37947
C;Accession: S32763; I37947
F;Kruppa, G.; Fuetterer, A.; Lemke, H.; Kroenke, M.
submitted to the EMBL Data Library, April 1993
A;Description: Cloning and characterization of TAF, a novel transactivating protein.
A;Reference number: S32763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::|| |::|
1065 EAVELEAKEVLKKLPPKVSVPSNLSYGEWLHGFEKKAKE-----CMAGTSGSEEVK---- 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 KDYEES-SW-----DSESL---CETVSQKDVCLPKATHQKEIDKINGKLEESPDNDGFL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDLANTGKWLQDLQEENESLKAHVQEVAQHN--LKEASSASQFEELEIVLKEKGNELKRL 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 LELK---NEQTLRADQMFPSESKQKNVEENSWDS-ESLRETVSQKDVCVPKATHQKEMDK 303
1923 QFDSLQ----BQKPSVVHENEHVRSVCVDLTFSRDSEQIVSDVIAAEVGYDEDECS 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MOKSVPNKALELKNEQTLRADEILPSESKOKDYEESSWDSESLCETV----SQKDVC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 KAPCRMKVS-IPTKALELMDMQ------TFKAEPPEKPSAFEPAIEMQKSVPNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 ISGKLEDSTSLSKIL------DTIHSCE-RARELQKDHCEQCTGKMEQMKKKFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LPKAAHQKEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKAL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 8.2%; Score 168; DB 2; Length 1356; Local Similarity 22.5%; Pred. No. 0.068; Lose 100; Conservative 83; Mismatches 153; Indels 108;
                                                                                                                                                                                                                                                                                                                                                             A;Accession: S32763
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1356 (KRU)-
A;Cross-references: UNIPROT:Q86UP2; EMBL:Z22551
B;Futterer, A.; Kruppa, G.; Kramer, B.; Lemke, H.; Kronke, M.
Mol. Biol. Cell 6, 161-170, 1995
A;Title: Molecular cloning and characterization of human kinectin.
A;Reference number: 137947; MUID:95306853; PMID:7787243
A;Accession: 137947
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hypothetical protein F5E19_70 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
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|116 VLEHKLKEADEMHTLLQLECEKYK 1139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-1356 < RES>
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Best Local Si
Matches 100;
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*Residues: 1-2109 <LEO>
A;Cross-references: UNIPROT:Q8ISF7; UNIPROT:Q8ISF6; UNIPROT:Q8ISF5; EMBL:AF067951; PIDN:
A;Experimental source: strain Bristol N2; clone H05009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1695 QADVPKVAAPLEQIQQEVEWWAAPLEPIQEEVPKEAAPSEPTQEDVPKGAAPLEPTQE 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1649 PTQADVPKVAAPLEQSQIQQ------EVPTVA---APSEPTQADVPKEAAPSEPS 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
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                                                                                                                                                                                                                                                                                                                                                                     279 ESLRETVSQ-----KDVCVPK-ATHQKEMDKISGKLEDSTSL-----SKILDTIHSCE 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AHOKEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKALELMDMQTFKAEPPEKPSAFEPA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IEMQKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESLRETVSQ-----SKILDTIHSCE 325
                                                     ----IEMQKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLCE 164
                                                                                                                                                             165 TVSQKDVCLPKATHQKEIDKINGKLEESPDNDGFLKAPCRMKVSIPTKALELMDMQTFKA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein H05009.1 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RARELOKDHCEQCTGKMEQMK--KKFCVLKKKLSEAKEIKSQLENOKVKWEQELCS 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MQKSVPNKALELKNEQTLRADEILPSESKQKDYBESSWDSESLCETVSQKD----VCLPKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.2%; Score 169; DB 2; Length 2109; 23.1%; Pred. No. 0.1; tive 77; Mismatches 173; Indels 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: intron positions not resolved (incomplete sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Accession: T33247
R.Leonard, S.; Hinds, K.
submitted to the EMBL Data Library, May 1998
A.Reference number: Z21308
A.Accession: T33247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Map position: 5
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C;Accession: T13030
R;Lantz, V.A.; Miller, K.G.
J. Cell Biol. 140, 897-910, 1998
A;Title: A class VI unconventional myosin is associated with a homologue of a microtubule A;Reference number: Z17588; MUID:98139549; PMID:9472041
A;Accession: T13030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   644 KKKSSAEIKQLNAYEIKVSKLEL-ELESTKQRFEEMTNNYQKEIENKKISEGKLLGEVEK 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 CVPKATHQKEMDKISGKLEDSTSLSKILDTIHSCERARELQKDHCEQCTGKMEQMKKKFC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-1690 <LAN>
A;Cross-references: EMBL:AF041382; NID:g2773362; PID:g2773363; PIDN:AAB96783.1
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                                                                                                                                                                                                                                                                                                                                               584 GDEVKCKLDKSEENARSIECEVLKKEKOMKILESKCNNLKKOVENKSKNIEELHQENKTL 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 -KSVPNKALELKNEQTLRAD----QMFPSESKOKN-----VEENSWDSESLRETVSQKDV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 QKDVCLPKAAHQ---KEIDKINGKLEGSPVKDGLLKANCGMKVSIPTKALELMDMQTFKA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SVPNKALELKNE-OTLRADEILP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E----ASDMALELKKHQEDIINCKKQEERLLKQIENLEEKEMHLRDELESVRKEFIQQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 SESKQKDYEESSWDSESL-CETV---SQKDVCLPKATH-QKEIDKINGKLEESPDNDGFL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microtubule binding protein D-CLIP-190 - fruit fly (Drosophila melanogaster) C; Species: Drosophila melanogaster C; Species: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VPNKALELKNEQTLRADEILPSESKQKDY-----BESSWDSESLCETVS----QKDVC
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                         1 8.0%; Score 164.5; DB 2; Length 993; Similarity 21.3%; Pred. No. 0.075; 33; Conservative 90; Mismatches 146; Indels 107;
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A;Molecule type: mRNA
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C;Keywords: cytoskeleton
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804 ILKDK--KDKKIQASL 817
                                                                                               93; Conservative
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                             Query Match
Best Local S
Matches 93
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                                                                     Me
                  C;Accession: T51505
R;Saro, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, B.; Kotani, H.; Tabata, S.; submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | : | | | | | : | | | : | | | : | | | DRSSPNSKSSVERRSPK-LPTPPEKSQARVAAVKGTESPQTTTRLSQIKEDLKKANERIS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSIPTKALELMDMOTFKAEPPEKPSAFEPAIEMOK--------SVPNKA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LELKNE-QTLR-----ADEILPSESKQKDYEE--SSWDSESLCETVSQ-KDVCLPKAT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAS-----VSLESVWKQLEGSNDKLHDTETEITDLKERIVTLETTVAKQKEDLEVSEQRL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 GKMEQMKKKFCVLKKKLISEAKEIKSQLE-----NQKVKWEQELCS-VRFLTLMKMKIIS 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87
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C;Date: 20-Peb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S49461; S59599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-993 <SAG>
A;Cross-references: EMBL:Z38118; NID:g1360015; PIDN:CAA86262.1; PID:g558603
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HQKEIDKINGKL------EESPDNDGFLKAPCRMKVSIPTKALELMDMQTFKAEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 KEKEMIVEKLANDLEAAKMAESNAHSLSNEW------OSKAKELEEQLEEANKLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EESSWDSESLCETVSQKDVCLPKAAHQKEIDKING-----KLEGSPVKDGLLKANCGMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.1%; Score 165.5; DB 2; Length 853; 23.1%; Pred. No. 0.055; Aztive 80; Mismatches 156; Indels 87;
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A; Description: Cloning and sequencing of the murine SCP1 cDNA.
A; Reference number: S49461
                                                                                                                                                                                                                                                                            A;Residues: 1-853 <SAT>
A;Cross-references: UNIPROT:Q9LFE4; EMBL:AL391147
A;Experimental source: cultivar Columbia; BAC clone F5E19
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Best Local Similarity
Matches 97; Conserv
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A; Molecule type: mRNA
A; Residues: 1-993 <UUL>
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A; Status: preliminary
                                                                                                                                                                         A, Accession: T51505
A, Status: preliminary
A, Molecule type: DNA
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A;Introns: 6/2; 79/3
A;Note: F5E19_70
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Length 1690; Indels

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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                               ---LESQKKSHN 1416
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                                                                                                                                                 DSESLRETVSQKDVCVPKATHQKEMDKISGKLEDSTSLSKILDTIHSCERARELQKDHCE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381 EEKLRTANEKLAEVLKEKEALEANVAEVTSNVATVTEV----CNELEEKLKTSDENFSKT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 VPNKALELKNEQTLRADEILPS-ESKQKDYEESSWDSESLCETVSQKDVCLPKATHQKEI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 DKINGKLEESPDNDGFLKAPCRMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIE--MQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 ELEGKKASESRFKEELSVLÓDLDAQTKGLÓAKLSEQEGINSKLAEELKEKELLESLSKDÓ 380
LCETVSQKDVCLPKATHQKEIDKINGKLESSPDNDGFLKAPCRMKVSIPTKALELMDMQT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 GKLEGSPVKDGLL----KANCGMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEMQKS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 KELNEKMSENEKVEAALKSSAGELAAVQE---ELALSKSRLLETEQKVSSTEALIDELTÖ 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: AE002093; NID: g6598483; PIDN: AAC69932.2; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                     probable myosin heavy chain [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F84730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 KSVPNKALELKNEQTLRADQMFPSESK--QKNVEENSWDSESLRETVSQKDVCVPKATHQ
                                ----EAAKLSGELQOVQEANGDIK-DSLVKVEELVKVLE----
                                                                       222 FKAEPPEKPSAFEPAIEMQKSVPNKALEL----KNEQTLRADQMFPSESKQKNVEENSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 ELK---NEQTLRADEILPSESKOKDYEESSWDSESLCETVSQKDVCLPKAAHQKEIDKIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.9%; Score 163; DB 2; Length 1269; 11.2%; Pred. No. 0.12; ve 86; Mismatches 169; Indels 50
                                                                                                                                                                                                                                            QCTGKMEQMKKKFCVLKKKLSEAKEIKSQLENQKVKWEQEL 377
                                                                                                                                                                                    ---ELKEALCOK-----ENGLKELQGKLDESNTV----
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Conservative 8
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A;Molecule type: DNA
A;Residues: 1-1269 <STO>
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Best Local Similarity
Matches 82; Conserv
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A,Map position: 2
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 162
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A; Molecule type: DNA
A; Residues: 1-216 < wARA-
A; Cross-references unippror: P08799; GB:M14628; GB:M1938; NID:g167834; PIDN:AAA33227.1; I
A; DeLozanne, A.; Lewis, M.; Spudich, J.A.; Leinwand, L.A.
B; DeLozanne, A.; Lewis, M.; Spudich, J.A.; Leinwand, L.A.
B; DeLozanne number: A24728; MUD:86016788; PMID:3901008
A; A; Reference number: A24728; MUD:86016788; PMID:3901008
A; A; Accession: A24728
A; Molecule type: mRNA
A; Residues: 2035-2116 < DEL>
B; Magle, G.; Noegel, A.; Scheel, J.; Gerisch, G.
R; Magle, G.; Noegel, A.; Scheel, J.; Gerisch, G.
R; Magle, G.; Noegel, A.; Scheel, J.; MUD:88112226; PMID:2828113
myosin heavy chain [similarity] - slime mold (Dictyostelium discoideum)
N;Contains: myosin ATPase (BC 3.6.4.1)
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text_change 09-Jul-2004
C;Accession: A26655, A24728; S00250
R;Warrick, H.M.; De Lozanne, A.; Leinwand, L.A.; Spudich, J.A.
Proc. Natl. Acad. Sci. US.A. 83, 9433-9437, 1986
A;Tille: Conserved protein domains in a myosin heavy chain gene from Dictyostelium discointeres number: A26655; WUID:87092266; PMID:3540939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: DNA
A, Residues: 1734-1893 - WAG>
C; Comment: The rod domain is highly periodic, containing a pattern of 7-residue repeats c
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide binding; P-loop; phosy
F; 19-181/Domain: globular head of HED>
F; 19-74/Domain: myosin motor domain homology < MMOT>
F; 19-186/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1474 CNS---AIKAKKTAESALESLKDEIDAANNAKAKAERKSKELEVRVAELEESLEDKSGTV 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1531 NVEFIRKKDA------EIDDLRARLDRETESRIKSDEDKKNTRKQFADLEAKVEEAQ 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1582 REVVTIDRLKKKLESDIIDLSTQLDTETKSRIKIEKSKKKLEQTLAERRAAEEGSSKAAD 1641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----STSLSKILDTIHSCERARELQKDHCEQCTGKMEQMKKKF---CVLKKKLSEAK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 PSAFEPAIEMQKSVPNKALELKNEQTLRADEILPSESKQKDYE-----ESSWDSES--- 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 LCETVSQKDVCLPKATHQKBIDKINGKL------ESPDNDGFLKAPCRMKVSIPT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KNVEENSW-----DSESLRETVSQKDVCVPKATHQKEMDKISGKLED-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KSVPN-KALELKNEQTLRADEILPSE-----SKQK---DYEESSWDSESLCETVSQKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 2116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68; Mismatches 173; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.9%; Score 163; DB;
23.4%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;819-2116/Domain: alpha-helical rod <ROD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S00250
A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 E----IKSQLENQKVK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.4%;
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Matches 103; Conservative
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myostelium discoideum
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18278; T30579
R;Hammer III, J.A.; Jung, G
J. Biol. Chem. 271, 7120-7127, 1996
A;Title: The sequence of the dictyostelium myo J heavy chain gene predicts a novel, dime:
A;Accession: T18278
A;Accession: T18278
A;Accession: T18278
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-2245 cHAM>
A;Residues: 1-2245 cHAM>
A;Residues: 1-2245 cHAM>
A;Cross-references: UMLPROT: P54697; EMBL: U42409; NID: g1150765; PID: g1150766; PIDN: AAA8516
B;Titus, M.A.; Kuspa, A.; Loomis, W.F.
Proc. Natl. Acad. Sci. U.S.A. 91, 9446-9450, 1994
A;Title: Discovery of myosin genes by physical mapping in Dictyostelium.
A;Reference number: Z20873; MUID: 95023928; PMID: 7937787
A;Accession: T30879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-190, F', 192-283, T', 285-290, R', 292-331, 'IE', 'WM', 337-338, 'LK', 342, 'YRMKS'
A;Cross-references: EMBL:L35322; NID:g1039360; PID:g1039361; PIDN:AAA79858.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1302 SLITQLTTVKFESTQVSTNVSHQKEKITTLKSTIEELNKSIGKLQAEQKNKD----- 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 AHQKEIDKINGKLEGSPVKDGLLKAN------CGMKVSIPTKALELMDMQTFKAEP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----IPTKALBLMDMQTFKAEPPEKPSAFEPAI-EMQKSVPNKALELKNEQTLRADQMF 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSESKOKNVEENSWDSESLRETVSOKDVCVPKATHOKEMDKISGKLEDSTSLSKILDTIH 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .........QCTGKMEQMKKKFCVLKK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---- PEKPSAFEPALEMOKSVPNKALELKNEQTLR-ADEILPSESKOK----DYEESSWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 NKALELKNEQTLRADEILPS----ESKQKDYEESSWD-SESLCETVSQKDVC---LPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SESLCETVSQKDVCLPKATHQKEIDKINGKLEESPDNDGFLKAPC-RMKVS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 257/3; 307/3
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP: P-10op
F;84-809/Domain: myosin motor domain homology <MMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.9%; Score 162.5; DB 2; Best Local Similarity 21.8%; Pred. No. 0.25; Matches 98; Conservative 73; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 KLSE-----AKEIKSQLENQKVKWEQEL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCERARELOKDHCE---
                                                                                                                                                 1233 V 1233
                                                                                          380 V 380
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A; Residues: 1-1938 «RES
A; Cross-references: UNIPROT: Q02566; GB: M76601; NID: G191623; PIDN: AAA37162.1; PID: G191624
A; Accession: 149463
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-193, 'D', 195-837,'S', 839-955,'N', 957-1938 «RE2>
A; Cross-references: GB: M76600; NID: G191621; PIDN: AAA37161.1; PID: G191622
A; Accession: 149462
                    alpha cardiac myosin heavy chain - mouse
C.Species: Mus musculus (house mouse)
C.Jate: O2-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
C.Accession: 149464; 149462; 149461; 149604
R.Quinn-Laquer, B.K.; Kennedy, J.E.; Wei, S.J.; Belsel, K.W.
A.Title: Characterization of the allelic differences in the mouse cardiac alpha-myosin layReference number: A38207; MUID:92250040; PMID:1577481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-544, 'A', 546-1938 < RE4>
A; Cross-references: GB:M76598; NID:g191617; PIDN:AAA37159.1; PID:g191618
R; Gulick, J.; Subramaniam, A.; Neumann, J.; Robbins, J.
Biol. Chem. 266, 9180-9185, 1991
A; Title: Isolation and characterization of the mouse cardiac myosin heavy chain genes.
A; Reference number: 149604; MUID:91225025; PMID:2026617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 -LMDMQTFKAEPPEKPSAFEPAIEMQKSVPNKALELKNEQTLRADQMFPSESKQKNVBEN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWDSESLRETVSQKDVCVPKATH----QKEMDKISGKLEDSTSLSKILDTIHSCERARE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 LQK--DHCEQCTGKME----QMKKK----FCVLKKKLISEAKEIKSQLENQKVKWEQELCS 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: 149462
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
Residues: 1-1938 <RE3>
Cross-references: GB:M76599; NID:g191619; PIDN:AAA37160.1; PID:g191620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M62404; NID:g192609; PIDN:AAA37424.1; PID:g192610 C;Superfamily: myosin heavy chain; myosin motor domain homology C;Keywords: ATP; cardiac muscle; heart; nucleotide binding; P-loop F;88-768/Domain: myosin motor domain homology <MMOT>. F;178-185/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77;
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                                                                                                                                                                                                                                                                                                                     Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: mRNA
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A; Status: translated
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Abt33260 Human tum
Ad193212 Human bre
Aaf17693 Human bre
Aai67217 B726P thi
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AAI67218
AAS47405
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AAF17693
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ABS64024
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ADL92840
                                                                                   AAF17980
AAI67223
AAS47410
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99US-00389681.
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23-JUN-1999;
02-SEP-1999;
03-NOV-1999;
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        Command line parameters:
-MODBLE_frame+_p1.mcd=1 - DEV=x1p
-MODBLE_frame+_p1.mcd=1 - DEV=x1p
-MODBLE_frame+_p1.mcd=1 - DEV=x1p
-De_Cgn12_1/USPTO_spool_p/US09489079/runat_01082005_141249_13290/app_query.fasta_1.1635
-De_Cgn12_1/USPTO_spool_p/US09489079/runat_01087IX=blosum62_-I-LOOPCL=0
-LOOPEXT=0 -UNITS=blits -START=1 - END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODBE_LOCAL_-OUTPMT=pco -NORM=ext -HEAPSIZE=500 -WINILRN=0 -MAXLEN=200000000
-USER=US09489079_@CGN 1 1 1418 @runat_01082005_141249_13290 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NGG_SCORES=0 -WATT -DSPELDCK=100 -LONGIGG
-DSV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Aai67216 B726P sec
Aas47122 Human cDN
Abc08777 Human bre
Abs63723 Human bre
                                                                                                                                                 August 1, 2005, 22:23:28; Search time 587.051 Seconds (without alignments) 3196.585 Million cell updates/sec
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                                                                                                                                                                                                                                                          1632
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- 2005 Compugen Ltd.
                                                                                                        - nucleic search, using frame_plus_p2n model
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Ygapop 10.0, Ygapext
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GlnLysLeuPheGlnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAla 260
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1. .540
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20-UUL-2000; 2000US-0219862P.
20-UUL-2000; 2000US-021300P.
18-DEC-2000; 2000US-0256592P.
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                                polypeptide useful for the treatment and diagnosis of tumors cancer comprises at least an immunogenic portion of a breast
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                                                                                                The present invention provides the coding sequences and some protein
                                                                                                           sequences of proteins associated with breast cancer in humans. These sequences can be used in the diagnosis and treatment of cancers,
                                                                                                                                                     0 U; 0 Other;
                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                     Sequence 1665 BP; 690 A; 289 C; 311 G; 375
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                                                                            Claim 6; Page 143; 238pp; English
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                               An isolated polypeptide e.g. breast cancer comprtumor protein.
WPI; 2001-122627/13.
P-PSDB; AAB50243.
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Human cDNA clone B726P-74 encoding
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08-JUN-2000; 2000US-00590751.
22-JUN-2000; 2000US-00604287.
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colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver, gastric, kidney, bladder, pancreatic or endometrial cancer. The present sequence represents a cDNA encoding a B726P second splice variant
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genic protein; breast antigen; breast antigen-related DNA; vaccine;
cancer; adoptive immunotherapy; tumour-reactive T-cell; cancer;
                                             Human breast antigen-related nucleotide #175
                                                                                                     Homo sapiens
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                                                                                          LeuHisGluAsnCysMetLeuLysLysGlulleAlaMetLeuLysLeuGlulleAlaThr
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The invention comprises a protein which contains an immunogenic portion of a breast antigen. The invention also comprises breast antigen-related has sequences. The protein of the invention is useful as a vaccine for inhibiting the development of breast cancer. The protein of the invention is used in adoptive immunotherapy for the treatment of cancer, and a pererating tumour-reactive T-cells which can be administered to a patient. The present DNA sequence represents a human breast antigenrelated nucleotide of the invention
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GAAAAGAATGCTGAACTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGG
                    LysLeuLysGluLysGluAspLysGluIleLeuGluAlaGluIleGluSerHisHisPro
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              AlaSerGlnTyrSerGlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSer
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The invention relates to an isolated breast tumour polynucleotide and the polypeptide it encodes. The polynucleotide and polypeptide are useful for detecting the presence of breast cancer in a patient, and in pharmaceutical compositions for treating breast cancer. The sequences are useful for stimulating an immune response in a patient and can therefore be used in production of vaccines. The sequences are also useful for detecting the presence of a cancer in a patient, by obtaining a biological sample with a composition of the invention and detecting the biological sample with a composition of the invention and detecting the amount of polynucleotide that hybridizes to the sample. This sequence represents a human breast
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23-JUN-1999; 99US-00339338.
02-SEP-1999; 99US-00389681.
03-NOV-1999; 99US-00433826.
17-APR-2000; 2000US-00551621.
08-JUN-2000; 2000US-00590751.
22-JUN-2000; 2000US-00604287.
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               AGTACGATATATAACAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCC
                                                                                   ProAlaPheHisIleAlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSer
                                        SerThrIleTyrAsnAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSer
                                                                          LysSerLeuLys1leAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuVal
                                                                                                            SerGluHisAlaGlnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHis
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Hepler WT, Henderson RA,
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Mcneill PD, Durham M;
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07-DEC-2001; 2001US-00007805.
13-FEB-2002; 2002US-00076622.
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Vedvick TS,
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                                  The invention comprises a method of stimulating and/or expanding T cells specific for a tumour protein. The invention further comprises human nucleic acids and proteins that are associated with tumours (e.g. breast cancer). The method and sequences of the invention are useful for stimulating and/or expanding T cells specific for a tumour protein, abatecting the presence of cancer, stimulating an immune response in a patient and treating breast cancer. The present DNA sequence represents a human tumour-related DNA sequence
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Example 1; Page 208-209; 375pp; English.
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                                               HisLysLysAlaAspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLys
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2000US-0051621.
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13-APR-2001;
07-DEC-2001;
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23-JUN-1999;
02-SEP-1999;
03-NOV-1999;
17-APR-2000;
08-JUN-2000;
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Conservative:
Mismatches:
Indels:
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                                                    US-09-489-079-25 (1-317) x ADL92840 (1-1665)
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                       Query Match:
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RESULT 8 ADE44130

1665 317

Length: Matches:

2.1e-136 1632.00

us-09-489-079-25.rng

Wed Aug

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Novel isolated polypeptide comprising immunogenic portion of breast tur
protein or its variant, useful for formulating vaccines for inhibiting
cancer development in a patient.
                                                           cell stimulator;
                                                                                                                                                                                                                                       Harlocker SL;
                                                     88; gene; breast tumour; cancer; vaccine; T
expander.
                                           Human cDNA associated with breast cancer #175
                                                                                                                                                                                                                                       Χu J,
                                                                                                                                                                                                                                                                                                         Claim 5; SEQ ID NO 178; 217pp; English.
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ВР
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99US-00285480.
99US-00339338.
99US-00389681.
99US-00433826.
ADE44130 standard; cDNA; 1665
                                                                                                                             17-APR-2000; 2000US-00551621
                              (first entry)
                                                                                                                                                                                        JIANG Y.
DILLON D C.
MITCHAM J L.
XU J.
HARLOCKER S L
                                                                                                                                                                                                                                       Y, Dillon DC,
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                                                                                                US2003104366-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer
                                                                                  Homo sapiens
                                                                                                                                                    02-APR-1999;
23-JUN-1999;
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03-NOV-1999;
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                              29-JAN-2004
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               ADE44130
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(XUJJ/)
(HARL/)
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(DILL/)
                                                           human;
T cell
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The invention relates to an isolated polypeptide comprising at least an immunogenic portion of a breast tumour protein. The polymucleotide, its polypeptide, its antibody, a pharmaceutical composition comprising the fusion protein or the polymucleotide encoding it, an isolated T cell the fusion protein or the polymucleotide encoding it, an isolated T cell population comprising T cells specific for a breast tumour protein, and a method for removing tumour cells from a biological sample is useful for inhibiting the development of a cancer in a patient. The polypeptide is useful for stimulating and/or expanding T cells specific for a breast tumour protein. Stimulating and/or expanding T cells specific for a breast cumour protein. Stimulating for inhibiting the development of a cancer in a patient. The method additionally involves the step of cloning at least one proliferated cell and then administering the cloned T cells to the patient. The present sequence represents a cDNA associated with Sequence 1665 BP; 690 A; 289 C; 311 G; 375 T; 0 U; 0 Other;

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1665
317
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                             (1-1665)
                                              US-09-489-079-25 (1-317) x ADE44130
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Percent Similarity: Best Local Similarity:

Alignment Scores:

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                                                            GCATCTCAATATAGTGGGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCT
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        MetGlnHisHisHisLeuLeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeu

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                                                                                                            GAAAAGAATGCTGAACTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGG
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LeuHisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThr
                                                                                                                                              AlaSerGlnTyrSerGlyGlnLeuLy8ValLeuIleAlaGluAsnThrMetLeuThrSer
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        ArgleualaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGlu

                                                                                                 AGACTGGCTTCTGCTGTACAAGACCATGATCAAATTGTGACATCAAGAAAAGTCAAGAA
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1054 GCATCTCAATATAGTGGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCT
                                      SerThr11eTyrAsnAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSer
                                                                                                                                                                                                         AGTACGATATATAACAATGAGGTGCTCCATCAACCACTTTCTGAAGGTCTCAAAGGAAATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention related to a combination of polynucleotides. The combination of polynucleotides is useful for preparing a composition for diagnosing or treating cancer or neurodegenerative disorders. The present sequence represents the human breast cancer diagnostic marker cDNA Incyte
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                                                                                           = (pos:269. .271, aa:Gly)
= (pos:278. .280, aa:Val)
= (pos:281. .283, aa:Lya)
= (pos:290. .292, aa:Lya)
= (pos:290. .292, aa:Luy)
= (pos:302. .310, aa:Gly)
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                                       Location/Qualifiers
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P-PSDB; ADB83983.
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(MAHI/) MAHINI B.
(WALK/) WALKER M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetic subtraction; DNA microarray analysis; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying tissue (tumor)-specific polynucleotides overexpressed in tissue of interest as compared to control tissue, for detecting cancer cells in patient, comprises DNA microarray analysis or quantitative polymerase chain reaction.
                                                                                                                                                            HisLysLysAlaAspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLys
                                                                                                                                                                                                                                                                             MetGlnHisHisLeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeu
                                                    241 GlnLysLeuPheGlnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 107-108; 127pp; English.
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20-UUL-2000; 2000US-0219862P.
27-UUL-2000; 2000US-0221300P.
18-DEC-2000; 2000US-0221300P.
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                                                                                                     An isolated polypeptide useful for the treatment and diagnosis of tumors e.g. breast cancer comprises at least an immunogenic portion of a breast
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                                                                                                                                                                                                                                                                             The present invention provides the coding sequences and some protein sequences of proteins associated with breast cancer in humans. These sequences can be used in the diagnosis and treatment of cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2307 BP; 919 A; 409 C; 439 G; 540 T; 0 U; 0 Other;
     Harlocker SL;
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     Mitcham JL,
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     Dillon DC,
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US-09-489-079-25 (1-317) x AAS47410 (1-2307)
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22-JUN-2000; 2000US-00604287.
20-JUL-2000; 2000US-00620405.
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The invention relates to isolated breast tumour proteins and nucleic acids that encode them, including immunogenic fragments of the proteins. Also included are expression vectors expressing the proteins. transformed cells and antibodies raised against the proteins or an antigen presenting cells and antibodies raised against the proteins or an antigen presenting in the protein. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate breast tumour protein expression, i.e. breast tumours and breast cancer e.g by gene therapy. The nucleic acids and their complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The proteins, nucleic acids and antibodies may be used in assays to identify conceins, nucleic acids and antibodies may be used to down activity. The antibodies and antagonists and antagonists and cated as diagnostic agents for detecting the presence of the proteins in samples capitates expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immunocorput tumour contains the present sequence is a cDNA from a breast tumour contains against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepler WT;
Human cDNA clone 19310.seq_B726P encoding a breast cancer protein.
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                                                                                                       ss; breast cancer protein; tumour; cancer; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated breast tumour polynucleotide and the polypeptide it encodes. The polynucleotide and polypeptide are useful for detecting the presence of breast cancer in a patient, and in pharmaceutical compositions for treating breast cancer. The sequences are useful for stimulating an immune response in a patient and can therefore be used in production of vaccines. The sequences are also useful for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with a composition of the invention and detecting the amount of polynucleotide that hybridizes to the sample. This sequence represents a human breast
                                                                                                                                                                                                                                                                                                                                                                                       Novel breast cancer polynuclectides and polypeptides encoded by the polynuclectides, useful for detecting the presence of breast cancer in a patient, and in pharmaceutical compositions, for treating breast cancer.
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              gene;
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02-APR-1999; 99US-00285480.
23-JUN-1999; 99US-003338.
02-SEP-1999; 99US-00338681.
03-NOV-1999; 99US-0043826.
17-APR-2000; 200US-00551621.
08-JUN-2000; 200US-005505151.
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                                                     Homo sapiens
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                                                                             TTACATGAAAATTGCATGTTGAAAAGGAAATTGCCATGCTAAAACTGGAAATAGCCACA
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Mitcham JL, Xu J, Harlocker SL, Hepler WT, Henderson RA,
Vedvick TS, Mcneill PD, Durham M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated breast cancer-associated polypeptide. The polypeptide may be used for the diagnosis and treatment of breast cancers. The methods are useful for detecting the presence of a cancer in a patient and treating a cancer in a patient. The present sequence represents cDNA encoding a human breast cancer-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140
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                                                                                                                                                                                                                                                                                                                                                  ATGGGAACAAGAGCTCTGCAGTGTGAGGTTTCTCACACACTCATGAAAATGAAAATTATCTC
                                                                                                                                                                                                                                                                                                                                                                                            GAAAAGAATGCTGAACTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysLeuLysGluLysGlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgleuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGACTGGCTTCTGCTGTACAAGACCATGATCAAATTGTGGACATCAAGAAAAAGTCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysSerLeuLys11eAsnLeuAsnTyrAlaG1yAspAlaLeuArgG1uAsnThrLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerGluHisAlaGlnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetTyrGlnAsnGluGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnLysLeuPheGlnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAla
                                                                                                                                                                                                                                                                                                                                MetGlyThrArgAlaLeuGlnCysGluValSerHisThrHisGluAsnGluAsnTyrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluLysAsnAlaGluLeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArg
                                                                                                                       Other;
                                                                                                                                                                     2307
317
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Matches:
Conservative:
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

August 1, 2005, 22:05:16 ; Search time 88.6398 Seconds (without alignments) 1831.334 Million cell updates/sec Run on:

US-09-489-079-25 1632 1 MGTRALQCEVSHTHENENYL......NHLKNRIYQYEKEKAETENS 317 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	Ω	29BXX3	6ISN6C	Q6ZR14	09н101	9Sdn6Ö	060311	Q69ZS2	9н0н6	D68DM0	Q81ZM7	Q9HCD1	AN18_HUMAN	Q9BXX2	Q6ZU57	6XI96 Ö	Q6ZU74	28NF67	Q8TDH5	фатрие в	075340	MLP1_YEAST	$\overline{0}6\overline{X}1\overline{Y}7$	QEDCAS	Q6RT24	MYHB CHICK	Q869R0	27XXP7	MYHB RABIT	MYHB MOUSE	92X3	076329
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٠	Query Match	97.2	77.1	50.2	50.2	50.2	41.0	38.7	34.6	34.1	33.9	33.5	30.5	25.2	20.5	16.3	15.3	13.0	13.0	12.4	11.8	11.4	11.2	11.2	11.1	11.1	11.0	10.9	10.9	10.8	10.8	10.7
	Score	1586	1258	819.5	819.5	819.5	699	632	265	556	552.5	546.5	497	411	334	266.5	250.5	212.5	212	202	192	186.5	183.5	183	181.5	180.5	179.5	177.5	177.5	176.5	176.5	175
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Q86KX8 Q7KT48	C190 DROME NIN HUMAN Q81JKO Q6BFFO	Q9C7V7 Q6PPZ7 Q86XU5	MYH9_HUMAN Q7Z6 <u>5</u> 9 Q8R384	TRIA HUMAN Q14981
999	7 7 7 7	0 0 0	- 77	7 7
1781	2090 1005 1602	555 813 1374	1960 724 1972	1979 2101
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332	3 3 3 4 3 4 3 4	38 39 40	4 4 4 4 3	44 45

ALIGNMENTS

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Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.S.,
Tayoda A., Ishii K., Totoki Y., Choi D.K., Soeda E., Ohki M.,
Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Reichwald K., Rump A., Schlilhabel M., Schudy A., Zimmermann W.,
Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shinizu N., Nordsiek G., Hornischer K., Brandt P.,
Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,
Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Lehrach H., Reinhardt R., Yaspo M.L.;
EMBL; All63203; CAB90394.1; --
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1213 YAGDALRENTLVSEHAQRDQRETQCQMKEAEHMYQNBQDNVNKHTBQQHGLDQKLFQLQS\1272
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                             249 KNWWLQQQLVHAHKKADNKSKITIDIHFLERKWQHHLLKEKNEEIFNYNNHLKNRIYQYE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 TLKLKEESLIKRASQYSGQLKVLIAENTMLISKLKEKQDKEILEAEIESHHPRLASAVQD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 TLKLKQKTLTKRASQYREQLKVLTAENTMLTSKLKEKQDKEILETEIESHHPRLASALQD 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNMWLQQQLVHAHKKADNKSKITIDIHFLERKMQHHLLKEKNEEIFNYNNHLKNRIYQYE 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 HDQSVTSRKNQELAFHSAGDAHLQGIMDVDVSNTIYNNEVLHQPLYEAQRKSKSPKINLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 YAGDDLRENALVSEHAQRDRCETQCQMKKAEHMYQNEQDNVDKHTEQQESLEQKLFKLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50038 MW; C6E704795C534625 CRC64;
                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Mismatches
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                                                                                                                                                                                    PRT;
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252; Conservative
                                                                                                                                                                                    PRELIMINARY;
                                                                                                       424
                                                                                    KEKAETENS 317
                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
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Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,

Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,

Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,

Sugiyama T., Irie R., Otsui T., Sato H., Ota T., Wakamatau A.,

Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,

Kimra K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,

Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

Suzuki Y., Sugano S., Nagahari K., Genbank/DDBJ databases.

BNBL, AK128577; BAC87568.1;

NON TER

SEQUENCE 1080 AA; 126741 MW; 478BAAA933AES95C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        628 SKINSLEIEFHHTRDALREKTLGLERVQKDLSQTQCQMKEMEQKYQNEQVKVNKYIGKQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKSKSLKINLNYAGDALRENTLVSEHAQRDQRETQCQMKEAEHMYQNEQDNVNKHTEQQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGTRALQCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                               Eukaryota; Metazena; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
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Catarrhini; Hominidae; Homo.
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Bird C.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 819.5; DB 2;
; Pred. No. 3.3e-36;
50; Mismatches 88;
PRT; 1080 AA
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                                                                                                Hypothetical protein FLJ46736.
Homo sapiens (Human).
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sest Local Similarity 54.09
Atches 177; Conservative
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PRELIMINARY;
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Homo sapiens (Human)
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=9606;
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                  06ZR14;
Q6ZR14
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1076 SKINSLEIEFHHTRDALREKTLGLERVQKDLSQTQCQMKEMEQKYQNEQVKVNKYIGKQB 1135
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                                                                                                                             EKNAELOMTLKLKEESLIKRASQYSGQLKVLIAENTMLTSKLKE-KQDKEILEAEIESHH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 CRLAAAVRDCDQSQTARDLKLDFQRTRQEWVR-----LHDKMKVDMSGLQAKNEILSEK 275
                                                                                                                                                                              61 EKNABLOMTLKLKBESLTKRASQYSGQLKVLIAENTWLTSKLK-EKQDKEILEABIBSHH 119
                                                                                                                                                                                                                                                      120 PRIASAVQDHDQIVTSRKSQEPAFHIAGDAC--LQRKMNVDVSSTIYNNEVLHQPLSEAQ 177
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                                                                                                        1 MGTRALQCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILK 60
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                                                                                                                                                                                                                                                                                                                            178 RKSKSLKINLNYAGDALRENTLVSEHAQRDQRETQCQMKEAEHMYQNEQDNVNKHTEQQE
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Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:31-39(1998).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                   Length 1715;
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                                                                      88; Indels
1715 AA; 196962 MW; A82858F5F58E3203 CRC64;
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Last annotation update)
                                   DB 2;
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46.1%; Pred. No. 2.4e-28;
tive 59; Mismatches 95;
                                  50.2%; Score 819.5; DB 2
54.0%; Pred. No. 5.5e-36;
ive 50; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKNEELFNYNHLKNRIYQYEKEKAETE 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIAA0565 protein (Fragment)
Name=KIAA0565;
                                   Query Match
Best Local Similarity 54.0%
Matches 177; Conservative
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Matches 152;
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SEQUENCE
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MEDITARE-9391452; PubMed=10470851;
KIKUND R., Nagase T., Ishikawa K., Hirosawa M., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIV.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 6:197-205(1999).
                                                                                                                                                                                                                                                                             1 MGTRALQCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILK
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                                                                                                                                                                                                                                       13; Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                      Length 1710;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                 1710 AA; 196409 MW; 01CBF9BADB894872 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                   Query Match 50.2%; Score 819.5; DB 2; Best Local Similarity 54.0%; Pred. No. 5.5e-36; Matches 177; Conservative 50; Mismatches 88;
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Pfam; PF00023; Ank; 4.
PRINTS; PR01415; ANKTRIN.
SMART; SM00248; ANK; 4.
PROSITE; PS50088; ANK_REPEAT; 4.
ANK_repeat.
1 1
                                                                       PRINTS; PRO1415; ANKYRIN.
SMART; SMORJEB, ANK; 4.
PROSITE; PS5008B; ANK REPEAT; 4.
PROSITE; PS50297; ANK_REP_REGION; 1.
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
     EMBL; AL162272; CAC19649.1;
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Name=KIAA1074;
                    HSSP; P20749; 1K1B.
InterPro; 1PR002110; ANK.
Pfam; PF00023; Ank; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 PRLASAVQDHDQIVTSRKSQEPAFHIAGDAC--LQRKMNVDVSSTIYNNEVLHQPLSEAQ 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLDOKLFOLOSKNWWLQQQLVHAHKKADNKSKITIDI-----HFLERKMQHHL-LK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGTRALQCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILK 60
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S., Okazaki N., Kikuno R.F., Ohara R., Kaisho T., Hoshino K., Kitamura H., Nagase T., Ohara O., Koga H., Koga H., Koga H., Chara O., Koga H., Koga H., Chara O., Koga H., Cangle Homologues of KIAA Gene: Iv. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous CDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries.";

DNA Res. 11:205-218(2004).

EMBL; AKI71096; BAD32374.1; -.

InterPro; IRR010989; L-snare.
LSEAORKSKSLKINLNYAGDALRENTLVSEHAQRDQRETQCQMKEAEHMYQNEQDNVNKH
                                              TEQQESLDQKLFQLQSKNMWLQQQLVHAHKKADNKSKI--TIDIHF-----LERKMQ
                                                                                                                                                                                                                                                                     Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.7%; Score 632; DB 2; Length 1043; 43.9%; Pred. No. 4.2e-26;
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1043 AA; 121354 MW; 5F37B1F9AA37B212 CRC64;
                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                              283 HHLLKEKNEEIFNYNNHLKNRIYQYEKEKA 312
                                                                                                           |:||:|::||:396 ILSLQEKNKELMDEYNHLKERMDQCEKEKA 425
                                                                                                                                                                                PRT; 1043 AA
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                                                                                                                                                                                                                                         MKIAA1074 protein (Fragment)
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Matches 144; Conservative
                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AL136793; CAB66727.1; -. HSSP; Q60778; 10Y3.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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40.7%; Pred. No. 1.3e-22;
ive 64; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50068; ANK REPEAT; 4.
PROSITE; PS50297; ANK REP RESIGNO; 1.
ANK repeat; Hypothetical protein.
ANK repeat; Hypothetical protein.
SEQUENCE 823 AA; 93968 MW; 9D2DDD5F52C379B2 CRC64;
                                                                            01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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823 AA
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                                                                                                                                                                                                          Hypothetical protein DKFZp434Al71
Name=DKFZp434Al71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002110; ANK. Pfam; PF00023; Ank; 6. PRINTS; PR01415; ANKYRIN. SMART; SMOR248; ANK; 6.
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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068DM
008DD
AC 068DJ
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349 QVSETDEKED-LIHENRLANDBIARLRLEKDTIKNQNLEK--KYLKDFEIVKRRGHEDLQK 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||| :|::|| || || || :| || :| || DHDQSHSSKRDQELAFQGTVDKCRHLQENLNSHVL-----ILSLQLSKABSKRVLKT 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NINYAGDALRENTLYSEHAQRDQRETQCQMKEAEHMYQNEQDNVNKHTEQQESLDQKLFQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOSKUMWLOQOLVHAHKKADNKSKITIDIHF-----LERKMOHH--LLKEKNEEIFN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |::|| ||||| | |||||::|
310 LKKQNMLLQQQLDDARNKADNQEKAILNIQARCDARVQNLQAECRKHRLLLEEDNKMLVN 369
254 BLHYTGEALKBKALVPEHVQSELKQKQSQMKDIEKMYKSGYNTMEKCIEKQE----RFCQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 EVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHOYQEKENKYFEDIKILKEKNAELOM
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                                                           LOSKNIMILOQQLVHAHKKADNKSKITIDIHF-----LERKMQHH--LLKEKNEBIFN
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brain which
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-20450683;
PubMed=10997877;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human in Prediction of the coding sequences of 100 new cDNA clones from looke for large proteins in vitro.";
DNA Res. 7:273-281(2000).
EMBL; AB046861; BAB13467.1; -.
NON TER
SEQÜENCE 718 AA; 82972 MW; 2AD05ADE70E3C97F CRC64;
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                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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42.2%; Pred. No. 1.1e-21;
ive 57; Mismatches 101;
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                                                                                                                                                                       370 ELNHSKEKECQYEKEKAERE 389
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                                                                                                                                          296 YNNHLKNRIYQYEKEKAETE 315
                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                             KIAA1641 protein (Fragment)
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                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                   Name=KIAA1641;
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AN18 HUMAN
ID AN18 H
AC Q8IVF6
DT 29-MAR
DT 29-MAR
DT 05-JUL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 NINYAGDALRENTLVSEHAQRDQRETQCQMKEAEHMYQNEQDNVNKHTEQQESLDQKLFQ 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTLVSEHAQRDQRETQCQMKEAEHMYQNEQDNVNKHTEQQESLDQKLFQLQSKNMMLQQQ 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 TLKLKBESLTKRASQYSGQLKVLIAENTMLTSKL-KEKQDKEILEAEIESHHPRLASAVQ 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQLKVLIABNTMLTSKLKEK-QDKEILEAEIESHHPRLASAVQDHDQIVTSR----
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                                                                                                                                                                                                                                                                                                   26 MLKKEIAMLKLEIATLKHOYQEKENKYPEDIKILKEKNAELQMTLKLKEESLTKRASQYS
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Bruno R., d'Orlando O., Altomonte A., Lamaj E., Maio M., Pucillo C.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

SEMBL; AF543495; AAN40505.1; -...

NON TER.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                            24;
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                                                                                 Koehrer K., Beyer A., Mowes H.W., Weil B., Amid C., Osanger Pobo G., Han M., Wiemann S.; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases. EMBL, CR749347; CAH18200.1; -. Hypothetical protein. SEQUENCE 292 AA; 34997 MW; FBD10B00B7173F1D CRC64;
                                                                                                                                                                                                                        Length 292;
                                                                                                                                                                                                                                                               84; Indels
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                    Query Match

34.1%; Score 556; DB 2;
Best Local Similarity 43.8%; Pred. No. 1.3e-22;
Matches 130; Conservative 59; Mismatches 84
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01-MAR-2003 (TrEMBLrel. 23, Last sequenc)
01-MAR-2003 (TrEMBLrel. 23, Last annotate)
Melanoma-associated antigen (Fragment).
                            SEQUENCE FROM N.A.
TISSUE-Testis;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 42.5$
Matches 136; Conservative
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310 EKSVRLNEKMITKTVARYSQQLNDLKAENARLNSELEKEKHNKERLEAEVESLHSSLATA 429
                                                                                                                         LOSKNWWLQQQLVHAHKKADNKSKITIDIH--FLERKWQHHLLKEKNEEIFNYNNHLKNR 303
                                                                                                                                                                                                                                                                                                                                                         Jaeger D., Stockert E., Guere A.O., Scanlan M.J., Karbach J., Jaeger D., Stockert E., Guere A.O., Chen Y.T.;
Jaeger E., Knuth A., Old L.J., Chen Y.T.;
Identification of a Tissue-specific Putative Transcription Factor in Breast Tissue by Serological Screening of a Breast Cancer Library.";
Cancer Res. 61:2055-2061(2001).
EMBL; AF269088; AAK27326.1; -.
HSSP; O75832; 1UOH.
InterPro; IPR02110; ANK.
Fram; PP00023; Ank; 3.
SMART; SM00248; ANK; 3.
                                                                                                                                                                                                       186 NILNYAGDALRENTLVSEHAQRDQRETQCQMKEAEHMYQNEQDNVNKHTEQQESLDQKLFQ
                                                                                                                                                                                                                                                              489 KLRETRDALREKTLALGSVOLDLRQAQHRIKEMKOMHPNGEAKESQSIGKONSLEERIRQ
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1011 AA; 114250 MW; 16627D7B218DE438 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ43983.
Homo seaplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Breast cancer antigen NY-BR-1.1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         976 TLKLKQKTVTKRASQYREQLKVLTAENTMLTSKLKE 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 TLKLKEESLTKRASQYSGQLKVLIAENTMLTSKLKE
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PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21174979; PubMed=11280766;
                                                                                                                                                                                                                                                                                                                                                                                                                                              304 IYQYEKEKAETE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       607 LLÓCEKEKAERE 618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 QMTLKLKEESLTKRASQYSGQLKVLIAENTMLTSKL-KEKQDKEILEAEIESHHPRLASA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 OCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILKEKNAEL 66
                                                                                                                                                                                                                                                                 Nagase T., Kikuno R., Ohara O.;
"The nucleotide sequence of a long cDNA clone isolated from human.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Prostate; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 K -> E (in Ref. 2).
88 Missing (in Ref. 2).
115664 MW; B9B288F087340D9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL; BC056266; AAH56266.1; ALT_TERM.
Genew; HGNC:23643; ANKRD18A.
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PROSTITE; PSS01297; ANK_REP_REGION; 1.
PROSTITE; PSS0088; ANK_REPEAT; 4.
ANK_repeat; Repeat.
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ANK 3.
ANK 4.
ANK 5.
   Ankyrin repeat domain protein 18A.
Name=ANKRD18A; Synonyms=KIAA2015;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-349 FROM N.A.
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Best Local Similarity 38.8%,
Matches 121; Conservative
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                                                               Homo sapiens (Human)
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199
130
288
992 AA;
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                            TISSUE=Brain;
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SOLUTION TO THE PROPERTY OF TH

68

REPEAT REPEAT

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us-09-489-079-25.rup

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TISSUE-Bone marrow;

X MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

X Alausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

R Brownstein M.J., Ugdin T.B., Toshlyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Nilalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Willialon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Williann A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Kraywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            155 MNVDVSSTIYNNEVLHQPLSEAQRKSKSLKINLNYAGDALRENTLVSEHAQRDQRETQCQ 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 MKEAEHMYQNEQDNVNKHTEQQESLDQKLFQLQSKNMWLQQQLVHAHKKADNKSKI--TI 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                    Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
Tanai H., Watanabe S., Ishida S., Ono Y., Hotura T., Watanabe M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagateuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 MKVDMSGLQAKNEILSEKLSNAESKINSLQIQLHNTRDALGRESLILERVQRDLSQTQCQ
                                                                                                                                                                                                                                                                                                                                                                                                     54; Indels 10; Gaps
Ŀukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primatea; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 DIHF------LERKMQHHLLKEKNEEIFNYNNHLKNRIYQYEKEKA 312
                                                                                                                                                                                                                                                                                                                                                             20.5%; Score 334; DB 2; Length 483; 45.8%; Pred. No. 2.1e-10; Live 27; Mismatches 54; Indels 1
                                                                                                                                                                                                                                                                                                 EMBL, AK125971; BAC86369.1; -.
SEQUENCE 483 AA; 56377 MW; EE47AEB54E1327E1 CRC64;
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Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 45.8% ses 77; Conservative
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                                                                                                   SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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1 MGTRALQCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILK 60
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                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                    61 EKNAELOMTLKLKEESLTKRASOYSGOLKVLIAENTMLTSKL-KEKQDKEIL 111
                                                                                                                                               Э,
                                                                                                              DB 2; Length 119;
                                                                                                        16.3%; Score 266.5; DB 2; Length 53.6%; Pred. No. 2e-07; ive 17; Mismatches 32; Indels
                 Strausberg R.; Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC007072; AAH07072.1; -. SEQUENCE 119 AA; 14172 MW; R06449B08455E397 CRC64;
                                                                                                                                                                                                                                                                                                                                                     Search completed: August 1, 2005, 22:22:14 Job time : 91.6398 secs
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 TISSUE=Bone marrow;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

August 1, 2005, 22:08:06; Search time 19.5308 Seconds (without alignments) 1561.672 Million cell updates/sec

US-09-489-079-25 1632 1 MGTRALQCEVSHTHENENYL......NHLKNRIYQYEKEKAETENS 317

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	·like	heavy	myosin heavy chain		c]e	interaptin - slime	microtubule bindin	unknown protein, 7	probable thyroid r	mitot	heavy		organe	heav	14					hypothetical prote	hyaluronan recepto	e L	, =	_	nonmuscle myosin I	•	giantin - human	centromere protein	myosin alpha heavy
SUMMARIES	ΙD	S38173	803166	A41604	JC5421	JC5420	T14867	T13030	C96667	T03719	A42184	A33977	A61231	T18372	S21801	T38435	T34081	A47297	B43402	C71622	E71606	JC4298	S26710	153799	S32763	A59282	152300	A56539	S28261	A46762
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م	Query Match	11.4	11.1	10.9	10.8	10.8	10.7	10.7	10.6	10.5	10.5	10.4	10.4	10.3	10.2	10.2	10.2		10.1	10.0	10.0	٠	9.9	9.9	•		9.9	6.6		9.8
	Score	186.5	180.5	177.5	176.5	176.5	175	174.5	173	172	172	170	170	168.5	167	166	166	165.5	165.5	164	163.5	163	161.5	161.5	161.5	161.5	161.5	161.5	160	159.5
	Result No.	-	8	m	4	S	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

early endosome ant tpr protein - huma	myosin heavy chain ninein - mouse	hypothetical prote MG328 homolog P01_	serine/threonine-s kinesin-related pr	transport protein	hypothetical prote protein V (fcrV) h	myosin II heavy ch	chromosome segrega	hypothetical coile	myosin-like coiled	hypothetical prote
A57013 S33124	A59252 T30171	T25410 S73693	S70633	\$67593	H70168	T47237	E89896	T38077	T50073	T34107
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7.6	9.7	6.0	و. و. ر	, o	0 0 4 4	. 4.	9.4	9.4	9.3	9.3
159	158.5	158.5	155.5	154	153.5	153	153	153	152.5	152
30	3 2 8	4 6	36	38	66.	4 4	42	43	44	45

ALIGNMENTS

	RESULT 1
	S38173 myosin-like protein MLP1 - yeast (Saccharomyces cerevisiae) N;Alternate names protein YKR055w; protein YKR415
	C;Decies: Saccharomyces Cerevisiae C;Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004
	C;Accebbion: 5501/3; 5*1001; 53120; R;Baladron, V.; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Esteban, P.F.; Garcia-Cantalejo, submitted to the Protein Sequence Database, March 1994
	A; Reference number: S38158 A; Accession: S38173
	A;Molecule type: DNA A:Residues: 1-1875 <bal></bal>
	A;Cross-references: UNIPROT:Q02455; EMBL:Z28320; NID:g486586; PID:g486587; MIPS:YKR095w
	R; Bou, G.; Esteban, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, M.; Jin
	Yeast 9, 1349-1354, 1993 A,Title: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae chromos
	A;Reterence number: S40644; MULD:94205255; FMLD:8154186 A;Accession: S40647
_	A; Molecule type: DNA
	A, Cross-references: EMBL:X73541; NID:g450550; PIDN:CAA51948.1; PID:g450554
	A, Experimental source: strain 2888C by September 1 by Manusa T. Chan R V . Rotatein. D.
	Mol. Gen. Genet. 237, 1993
	A;Title: A new yeast gene with a myosin-like heptad repeat structure. A:Reference number: S31207; MUID:93247549; PMID:8483450
	A; Accession: 831207
	A; Molecule Cype: DNA A; Residues: 1-300, 'A/, 302-1875 < KOE>
	A;Cross-rerences: EMBL:LU1992; NID:g1/1990; FIDN:AMA31/03:1; FID:g1/1990; C;Genetics:
	A;Gene: SGD:MLP1 A;Cross-references: SGD:S0001803; MIPS:YKR095w A;Map position: 11R
	11.4%
	Best Local Similarity 25.1%; Pred. No. 0.0077; Matches 82; Conservative 63; Mismatches 127; Indels 55; Gaps 13;
	Qy 6 LQCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILKEKNAE 65
	Qy 66 LQMTLKLKEBSLTKRASQYSGQLKVLIAENTWLTSKLKEK-QDKEILEAEIESHHPRLAS 124
,	DD 1279 VHRWKKRSQDILEKHEQLSSSDYEKLESEIENLKEELENKERQGAEAEKFNRLRR 1334
	Qy 125 AVQDHDQIVTSRKSQEPAFHIAGDACLQRKMAVDVSSTIYNNEVLHQPLSEAQRKSKSLK 184
	Db 1335 QAQERLKTSKLSQDSLTEQVNSLRDAKNVLENSLSEANARIEELQ 1379

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11.1%; Score 180.5; DB 1; ilarity 23.4%; Pred. No. 0.018; Conservative 62; Mismatches 145;
F;707,717/Active site: Cys #status predicted
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A;Residues: 1-1972 <BAB>
A;Cross-references: GB:M77812
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A;Residues: 1455-1972 <NAG>
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                                                                                              Local Similarity
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Matches
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Ja-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S03166; A27066; A26045; A36604; A31298
R;Yanagisawa, M.; Hamada, Y.; Katsuragawa, Y.; Imamura, M.; Mikawa, T.; Masaki, T.
J;Mol. Biol. 198, 143-157, 1987
A;Title: Complete primary structure of vertebrate smooth muscle myosin heavy chain deduct A;Reference number: S03166; MuID:8918918; PMID:2892941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: protein
A,Residues: 54-67;146-183 <ON2>
R;Cole, D.G.; Yount, R.G.
Biochemia, 13, 6186-6192, 1992
A;Title: Stability and photochemical properties of vanadate-trapped nucleotide complexes
A;Reference number: A43298; MUID:92329440; PMID:1385724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-1979 <YAN>
A;Residues: 1-1979 <YAN>
A;Cross-references: UNIPROT:P10587; EMBL:X06546; NID:g63633; PIDN:CAA29793.1; PID:g63634
A;Cross-references: UNIPROT:P10587; EMBL:X06546; NID:g63633; PIDN:CAA29793.1; PID:g63634
A;Note: part of this sequence was confirmed by protein sequencing
R;Maita, T.; Onishi, H.; Yajima, E.; Matsuda, G.
J. Biochem. 102, 133-145, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Amino acid sequence of the amino-terminal 24 kDa fragment of the heavy chain of A;Reference number: A27066; MUID:88032919; PMID:3312184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 653-855 <ONI>
R;Onishi, H.; Maita, T.; Matsuda, G.; Fujiwara, K.
B. Diol. Chem. 265, 19362-19368, 1990
A;Title: Lys-65 and Glu-168 are the residues for carbodiimide-catalyzed cross-linking A;Reference number: A36604; MUID:91035476; PMID:1977747
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A;Molecule type: protein
A;Residues: 169-183 <COL>
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; blocked amino end; coiled coil; hydrolase; methylated
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F;1291-1979/Domain: carboxyl-terminal <CBT>
F;1240-1979/Domain: carboxyl-terminal <CBT>
F;2/Modified site: blocked amino end (Ser) (in mature form) #status experimental
F;128/Modified site: NG,NG,NG-trimethyllysine (Lys) #status experimental
F;183/Binding site: ATP (Lys) #status predicted
                                                                     1380 -NAKVAQGNNQLEAIRK---LQEDAEKASRELQAKLEESTTSYESTINGLNEEITTLKEE 1435
                                                                                                                                                                                                                                  1436 IEKOROIOOOLOATSANEONDLSNIVESMKKSFEEDK----IKFIKEKTO----EVNEK 1486
                               ---KH 232
                                                                                                                                                                    233 TEQQESLDQKLFQLQSKNMWLQQQLVHAHKKADNKSKITIDIHFLERKWQHHLLKEKNEE 292
                               185 INLNYAG-----DALRENTLVSEHAQRDQRETQCQMKEAEHMYQNEQDNVN-
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A;Residues: 2,72',4-204 <MAI>
K;Onishi, H.; Maita, T.; Wanishi, T.; Watanabe, S.; Matsuda, G.
J. Biochem. 100, 1433-1447, 1986
A;Title: Amino acid sequence of the 203-residue fragment of the h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myosin heavy chain, gizzard smooth muscle [similarity] - chicken
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F;177-184/Region: nucleotide-binding motif A (P-loop)
F;565-578/Region: actin binding #status predicted
F;636-53/Region: actin binding #status predicted
F;850-1940/Domain: coiled coil <COI>
                                                                                                                                                                                                                                                                                                                                                                1487 ILEAQERLNOPSNINMEEIKKKWESEH 1513
                                                                                                                                                                                                                                                                                                     293 IFNYNNHL---KNRIYQYEKEKAETEN 316
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A;Experimental source: smooth muscle
A;Note: examination by Southern blotting for the regions of difference between this isofo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myosin heavy chain, smooth muscle, long splice form - rabbit

N. Contains: myosin ATPase (BC 3.5.4.1)

C. Species: Oryctolagus cuniculus (domestic rabbit)

C. Species: Oryctolagus cuniculus (domestic rabbit)

C. Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Apr-2002

C. Accession: A41604; A33501

R. Babij, P.; Kelly, C.; Periasamy, M.

Proc. Natl. Acad. Sci. U.S.A. 88, 10676-10680, 1991

Proc. Natl. Acad. Sci. U.S.A. 88, 10676-10680, 1991

A; Reference number: A41604; MUID:92073350; PMID:1961735
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C;Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methylated
F;88-771/Domain: myosin motor domain homology <MMOT>
F;178-185/Region: nucleotide-binding motif A (P-loop)
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J. Biol. Chem. 264, 9734-9737, 1989
A;Title: Identification of two types of smooth muscle myosin heavy chain isoforms by
A;Reference number: A33501; MUID:89255535; PMID:2722872
                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                           1361 BVEAKQNLERHISTLTIQLSDSKKKLQEFTATVETMEEGKKKLQREIESLTQQFEEKAAS 1420
                                                                                                                                                                                                                     | | : | | | : | | : | | | : | | | 120
1067 EGESSDIHE-----QIABLQAQIARLKAQLAKKEBELQAALARLEDETSQKNNALKKIR 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1241 DLANEIRSLSQAKQDVEHKKKKLEVQLQDLQSKYSDGERVRTELNEKVHKLQIEVENVTS 1300
                                                                                                                                                                                                                                                                                                                                   58 ILKEKNAELQMTLKLKEESLTKRASQ---YSGQLKVLIAE-----NTWLTSKLKEKQDK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EI-----LEARIESHHPRLASAVQDHDQIVTSRKSQEPAFHIAGDACLQRKMNVDVSST 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 IYNNEV--LHQPLSEAQRKSKSLKINL----NYAGDALRENTLVSEHAQRDQRETQ---C 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 -VHAHKKADNK-SKITIDIHFLERKMQHHLL-----KEKNEEIFNYNNHLKNRIYQ 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 OMKEAE-------HMYQNEQDNVNKHTEQGESLDQKLFQLQSKNMWLQQQL-- 257
                                                                                                                                                                 ---NKYFEDIK 57
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F;184/Binding site: ATP (Lys) #status predicted
Length 1979;
                                                                                  Indels
DB 1;
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F;633-647/Region: actin binding #status predicted
F;844-1338/Domain: coiled coil #status predicted
F;844-1284/Region: S2
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Smooth muscle myosin heavy chain 1 - mouse
C;Species: Mus musculus (house mouse)
C;Accession: JG5420
R;Hasegawa, K.; Arakawa, E.; Oda, S.; Matsuda, Y.
Biochem. Biochem. Biophys. Res. Commun. 232, 313-316, 1997
A;Title: Molecular cloning and expression of murine smooth muscle myosin heavy chains.
A;Reference number: JG5420; MUID:97242182; PMID:9125171
A;Accession: JG5420
A;Molecule type: mRNA
A;Residues: 1-1972 cHAS>
A;Residues: 1-1972 cHAS>
A;Residues: 1-1972 cHAS>
A;Cross-references: UNIPROT:006538; DDBJ:DB5923; NID:g1945077; PIDN:BAA19690.1; PID:g194f
A;Experimental source: smooth muscle
C;Comment: This protein plays a role in smooth muscle cell contraction.
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Reyvords: nucleotide binding; P-loop
F;88-771/Domain: myosin motor domain homology cMMOT>
F;178-185/Region: nucleotide-binding motif A (P-loop)
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277 ELSDKVHKLÓNEVESVTGMLNEAEGKAIKLAKDVASLGSQLÓDTÓELLQEETRÖKLNVST 1336
                                                                                                                                                                                                                                                                                                          1277 ELSDKVHKLONEVESVTGMLNEAEGKAIKLAKDVASLGSQLQDTQELLQEETROKLNVST 1336
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                                                                                                                LVSEHAQRDQRETQC---QMKEAE-------HMYQNEQDNVNKHTEQQESLDQ 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
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                                                                                                                                                                                                                                                                    242 KLFQLQSKNMWLQQQLVHAHKKADN----KSKITIDIHFLERKMQH-----HLLKEKNEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interaptin - slime mold (Dictyostelium discoideum)
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RjHasegawa, K.; Arakawa, E.; Oda, S.; Matsuda, Y.
Bjechem. Biophys. Res. Commun. 212, 313-316, 1997
A;Title: Molecular cloning and expression of murine smooth muscle myosin heavy chains.
A;Reference number: JC5420; MUID:97242182; PMID:9125171
A;Rocleanion: JC5421
A;Rocleule type: mRNA
A;Rocleule type: mRNA
A;Residues: 1-1938 «HAS>
A;Cross-references: UNIPROT:008638; DDBJ:D85924; NID:g1945079; PIDN:BAA19691.1; PID:g194
A;Cross-references: UNIPROT:o08638; DDBJ:D85924; NID:g1945079; PIDN:BAA19691.1; PID:g194
C;Comment: This protein plays a role in smooth muscle cell contraction.
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Superfamily: myosin motor domain homology whor>
F;Reyvorts: myosin motor domain homology whor>
F;178-185/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1104 AOKANNALKKIRELEGHISDLOEDLDSERAARNKAEKOKRDLGEELEALKTELEDTLDSTA 1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                       - KANLDKTKQTLEKENADLAGELRVLGQAKQEVEHKKKKLEVQLGQELQSKCSDGERARA 1276
                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTSKLKEKODKEI-----LEAEIESHHPRLASAVQDHDQIVTSRKSQEPAFHIAGDACL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRKMNVDVSSTIYNNE-----VLHQPLSEAQRKSKSLKINL----NYAGDALRENT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLFQLQSKNMWLQQQLVHAHKKADNK----SKITIDIHFLERKMQH--HLLKEKNEEIFN 295
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                                                                                                                                                                                                                                                                                                                                                                                        AELOMTLK-----LKEESLTKRASQYSG-----OLKVLIAE----NTM 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           emooth muscle myosin heavy chain 2 - mouse ('Species: Mus musculus (house mouse) ('Species: Mus musculus (house mouse) ('Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004 ('Accession: JG5421 ('Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 RALQCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILKEKN
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                                                                                                                                                                                                                                        4 RALQCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILKEKN
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                                                                                             Length 1972;
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                                                                                             DB 1;
                                                                                                                                                               66; Mismatches 141;
                                                                                         10.9%; Score 177.5; DB 21.5%; Pred. No. 0.026;
                   F;701,711/Active site: Cys #status predicted
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FOKEIESLTQQYEEKAA 1413
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Matches 85; Conservative
                                                                                                                                                                   Conservative
                                                                                                                                Local Similarity
                                                                                                                                                                   81;
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                                                                                                 Query Match
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C; Species: Dictyostelium discoideum C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 C; Accession: T14867 R; Rivero, F.J; Kuspa, A.; Brokamp, R.; Matzner, M.; Noegel, A.A. J; Cell Biol. 142, 735-756, 1998 A; Title: Interaptin, an actin-binding protein of the alpha-actinin superfamily in Dictyc Ls. A; Reference number: Z18248; MUID:98365468; PMID:9700162 A; Retauts: pre-liminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-1738 cRIV> A; Cross-references: UNIPROT:076329; EMBL:AF057019; NID:g3549260; PID:g3549261; PIDN:AAC3 C; Genetics: A; Gene: abpD A; Introns: 173/2; 1680/1	Qy 45 YQEKENKYPEDIKILKERNAELQMTLKLKEESLITKRASQYSGQLKVLIAENTM 97 Db 1201 AQGSEQKLQQSSQTSKEKITEAEIEQSLQDSVKQKEELVQNLEEKVRESSSIIEAQNTK 1260 Qy 98 LTSKLKEKQDKEILEAEIESHHPRLASAVQDHDQIVTSKKSQERAFHIAG 147 Db 1261 LNSENVQLENKTSCLKETQD-QLLESQKKEKQLQEEAAKLSG 1301 Qy 148 DACLQRKANVDVSSTIYNNEVLHQPLSE
Query Match 10.7%; Score 175; DB 2; Length 1738; Best Local Similarity 21.6%; Pred. No. 0.031; Matches 77; Conservative 74; Mismatches 103; Indels 102; Gaps 14; Qy 23 BNCMLKKBIAMLKLEIATLKHQYQEKENKYFEDIKILKEKNAELQMTLKLKES 76 I : : : : : 1 Db 1058 ENDLFEKENQIQQLQ-SQLNEQRQQSNQLSEKDQQLNQLIEKNESDQKEQQEKQQSIEN 1116	QY 243 LFQLQSKNAWLQQQLVHAHKKADNKSKITIDIHFLERKAQH-HLLKEKNEEIFNYNNHLK 301 Db 1422 LEQAQQKERTLQEETSKLAEQLSQLKQANEELQKSLQQKQLLLEKGNEFD 1471 QY 302 NRIYQYEKEKAETENS 317 E::::::::::::::::::::::::::::::::::::
77 -LTKRASQYSGQLKVLIAENTMLTSKL	RESULT 8 C96667 unknown protein, 71502-69704 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: C96667 C;Accession: C9667 C;Accession: M. F.; Ecker, J. R.; Palm, C. J.; Federspiel, N. A.; Kaul, S.; White, O.; Alonso, Chin, C. W.; Chung, M. K.; Conn, L.; Conway, A. B.; Conway, A. R.; Creasy, T. H.; Dewar, K.; ansen, N. F.; Hughes, B.; Huizar, L.
DD 1235SEKDEKLÖSIÜFENDEKEKÜLSEKDEKLÜŞIÜÇNENÜLENÜENVAĞPS 1284 QY 205 QRDQRETQCQMKEABHMYQNEQDNVNKHTEQQESLDQKLFQLQSKNMMLQQQLVHAHKKA 264 :: : :	Nature 400, 2009 10.000, 2009 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Status: Dreliminary
RESULT 7 T13030 microtubule binding protein D-CLIP-190 - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Species: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000 C;Accession: T13030 R;Lantz, V.A.; Miler, K.G. J. Cell Biol. 140, 897-910, 1998 A;Title: A class VI unconventional myosin is associated with a homologue of a microtubul	
A, Reference number: Z17588; MUID:98139549; PMID:9472041 A, Accession: T13030 A, Status: preliminary; translated from GB/EMBL/DDBJ A, Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: mRNA A, Residues: 1-1690 < LAN> A, Experimental tource: EMBL.AF041382; NID:92773362; PID:92773363; PIDN:AAB96783.1 A, Experimental source: strain Oregon R C, Genetics: A, GTOSS - references: FlyBase: FBGn0020503 C; Keywords: cytoskeleton	
Query Match Best Local Similarity 22.9%; Pred. No. 0.032; Matches 86; Conservative 59; Mismatches 138; Indels 93; Gaps 12; Qy 6 LQCEVSHTHBNENYLLHENCMLKKEIAMLKL	Db 227 STLEEVNRLQGQKNETEAELEREKQEKPALLNQIN-UVQKALLEQEAANTL 277 Qy 174 SEAQRKSKSLKINLNYACDALRENTLVSEHAQRORETCQM 215

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R;Tang, T.K.; Tang, C.C.; Chen, Y.L.; Wu, C.W.
J. Cell Sci. 104, 249-260, 1993
A;Title: Nuclear proteins of the bovine esophageal epithelium. II. The NuMA gene gives ri
A;Reference number: S33376
A;Rocession: S33376
A;Rocession: S33376
A;Rolecule type: DNA
A;Residues: 1705-2101
A;Resid
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A,Note: the authors translated the codon GAG for residue 781 as Gly, TTC for residue 1761
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NiContains: myosin AfPase (BC 3.6.4.1)
C;Species: Gallus gallus (chicken)
C;Species: J1-Dec.1993 #sequence_revision 31-Dec.1993 #text_change 09-Jul-2004
C;Date: 31-Dec.1993 #sequence_revision 31-Dec.1993 #text_change 09-Jul-2004
C;Accession: A33977; S06116; A44422
R;Shohet, R.V.; Conti, M.A.; Kawamoto, S.; Preston, Y.A.; Brill, D.A.; Adelstein, R.S.
Proc. Natl. Acad. Sci. U.S.A. 86, 7726-7730, 1989
A;Title: Cloning of the cDNA encoding the myosin heavy chain of a vertebrate cellular myc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Status: preliminary
A;Rolecule type: mRNA
J. Cell Biol. 116, 1303-1317, 1992
A;Title: NuMA: an unusually long coiled-coil related protein in the mammalian nucleus.
A;Rolecule number: S23647; MUID:92176231; PMID:1541630
A;Rolecule type: preliminary
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 ESHHPRLASAVQDHDQIVTSRKSQEPAFHIAGDACLQRKMNVDVSSTIYNNEVLHQPLSE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 AQRKSKSLKINLNYAGDALRENTLVS------EHAQRDQRETQCQMKEAEHMYQNE 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDNVNKHTEQQESLDQKLPQLQSKNMWLQQQLVHAHKKADNKSKITIDIHFLERKMQHHL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LQCEVSH----THENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|: | :::|:| | LEEQQRCISELKAETRSLVEQHKRERKELE 758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GDB:137229; OMIM:164009
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hes 80; Conservative
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C, Keywords: mitosis; nucleus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-771,'Q'
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A;Residues: 1-2101 <COM-
A;Cross-treferences: UNIPROT:Q14981; EMBL:Z11584; NID:g35120; PIDN:CAA77670.1; PID:g35121
A;Notes requence extracted from NCBI backbone (NCBIN:85755, NCBIP:85760)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-761 <ABE>
A;Cross-references: UNIPROT:Q15643; EMBL:AF011368; NID:g2618824; PIDN:AAB84386.1; PID:gd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blood 90, 4271-4277, 1997
A,Title: Pusion of the platelet-derived growth factor receptor beta to a novel gene
A,Reference number: 215027; MUID:98043615; PMID:9373237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YQNEQDNVNKHTEQQESLDQKLFQLQSKNMMLQQQLVHAHKK---ADNKSKITID 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 VDLEETVESLRNEVERKGDEIESLMEKMSNIEVKLRLSNQKLRVEQVLTEKEGELKRIE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 NENELLROAVTNIKERILILEMDIGKLKGENEKIVETYRGKETEY----OALQETNMKFS 303
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                                                                                                                                                                                                                                                                                                                                                        probable thyroid receptor interactor - human (fragment)
NiAlternate names: CEV14 protein
C;Species: Homo sapiens (man)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03719
R;Abe, A.; Emi, N.; Tanimoto, M.; Terasaki, H.; Marunouchi, T.; Saito, H.
Blood 90, 4271-4277, 1997
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C;Species: Homo sapiens (man)
C;Date: 3.1-Dec-1993 #text_change 09-Jul-2004
C;Accession: A64184; S33376; S55331; S23647; S24554
R;Compton, D.A.; Szilak, I.; Cleveland, D.W.
J. Gall Biol. 116, 1395-1408, 1992
A;Title: Primary structure of NuMA, an intranuclear protein that defines a A;Reference number: A42184; MUID:92176238; PMID:1541636
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                                                                                                                                268 SKITIDIHFLERKM-----QHHLLKEKNEEIFNYNNHLKNRIYQYEKEKAETEN 316
                                                                                                                                                                     274 I-----HFLERKMQHH------LLKEKNEEIFN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: T03719
A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
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A;Residues: 152, EAI', 56-659, T', 661-868, T', 870-930, C', 932-1239, KG', 1242-1337 <RES>
A;Cross-references: GB-M81105; NID:9188988; PIDN:AAA59888.1; PID:9553596
R;Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A;Title: Identification and overlapping expression of multiple unconventional myosin gent A;Reference number: ASS758; MUID:94294418; PMID:8022818
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A;Map position: 22q12.3-22q13.1
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Superfamily: myosin neavy chain; myosin motor domain motor domain; myosin motor domain homology cMMOT>
F;84-764/Domain: myosin motor domain homology cMMOT>
F;174-181/Region: nucleotide-binding motif A (P-loop)
F;552-565/Region: actin binding #status predicted
F;837-1938/Domain: colled coil #status predicted
F;837-1277/Domain: colled coil #status predicted cOI>
F;837-1277/Domain: S2 #status predicted coil
                                                                                                          Nighternate names: cellular myosin heavy chain; myosin type 9; NWMHC-A Nighternate names: cellular myosin heavy chain; myosin type 9; NWMHC-A Nicontains: myosin ATPase (BC 3.6.4.1) (Species: Homo sapiens (man) (Species: 12-May-1994 #sequence revision 14-Jul-1994 #text_change 09-Jul-2004 (Spacession: A61231; A34876; I52562; I61692 (Spacession: A61231; A34876; I52562; I61692 (Spacession: A); Wang, M.; McBride, O.W.; Kawamoto, S.; Yamakawa, K.; Gdula, D.; Adelstein, Circ. Res (Sp. 330-539; 1991) (A); Kawamoto, S.; Yamakawa, K.; Gdula, D.; Adelstein, A; Title: Human normuscle myosin heavy chains are encoded by two genes located on differer A; Reference number: A61231; MUID:91316803; PMID:1860190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P35579; UNIPROT:Q9UMJO; GB:M69180; NID:g189029; PIDN:AAA6176: R;Saez, C.G.; Myers, J.C.; Shows, T.B.; Leinwand, L.A. Proc. Natl. Acad. Sci. U.S.A. 87, 1164-1168, 1990 A;Title: Human nonmuscle myosin heavy chain mRNA; generation of diversity through alternative Human nonmuscle myosin heavy chain mRNA; generation of diversity through alternative A;Reference number: A34876; MUID:90138958; PMID:1967836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 715-1961 <SAE>
A; Residues: 715-1961 <SAE>
A; Cross-references: GB:M31013; NID:g189035; PIDN:AAA36349.1; PID:g189036
R; Toothaker, L.E.; Gonzalez, D.A.; Tung, N.; Lemons, R.S.; Le Beau, M.M.; Arnaout, M.A.;
Blood 78, 1826-1833, 1991
A; Title: Cellular myosin heavy chain in human leukocytes: isolation of 5' cDNA clones, chaiterence number: 152562; WUID:92003925; PMID:1912569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LESERASRNKAEKOKRDLGEELEALKTELEDTLDSTAAQQELRSKREQEVNILKKTLEEE 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A;Molecule type: mRNA
A;Residues: 182-218 <BEM>
A;Cross-references: GB:L29141; NID:g457249; PIDN:AAA20904.1; PID:g531134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1278-1961/Domain: light meromyosin #status predicted <LMM>
F;1939-1961/Domain: carboxyl-terminal <CBT-
F;125/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;180/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94;
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22.8%; Pred. No. 0.068;
tive 59; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 LKKEIAMLKLEIATLKHQYQEKENKYFEDIKILKEKNAELQMTLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                 myosin heavy chain nonmuscle form A - human
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les 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-715 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: A34876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: I52562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A61231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB: MYH9
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                                                                                                                  A;Residues: 1-1959 <SHO>
A;Residues: 1-1959 <SHO>
A;Cross-references: UNIPROT:P14105; GB:MZ6510; NID:g212382; PIDN:AAA48974.1; PID:g212383
A;Katsuragawa, Y.; Yanagisawa, M.; Inoue, A.; Masaki, T.
Eur. J. Biochem. 184, 611-616, 1989
A;Title: Two distinct nonmuscle myosin-heavy-chain mRNAs are differentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: myosin heavy chain; myosin motor domain homology (Keywords: actin binding; Arp; colled coll; hydrolase; methylated amino acid; nucleotid (Keywords) argonin motor domain homology <AMACTA (Domain: myosin motor domain homology <AMACTA (181/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S06116
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: GB:X17589
A;Cross-references: GB:X17589
A;Cross-references: GB:X17589
Call Biol. 118, 1085-1095, 1992
A;Title: Role of the COCH-terminal nonhelical tailpiece in the assembly of a vertebrate
A;Reference number: A43422; MUID:92381096; PMID:1512291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1900-1959 <HOD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1226 RAELSNEVKVLLOGKGDAEHKRKKVDAQLOELOVKFTEGERVKTELAERVNKLOVELDNV 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1286 TGLLNQSDSKSIKLAKDFSALESQLQDTQELLQEËTRLKLSFSTKLKQTEDEKNALKËQL 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SLKINLNYA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --KSKITIDIHFLERMOHHL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1278-1959/Region: light meromyosin
F;1978-1959/Domain: carboxyl-terminal <CBT>
F;1937-1959/Domain: carboxyl-terminal <CBT>
F;125/Modified site: N6.N6.N6-trimethyllysine (Lys) #status predicted
F;180/Binding site: ATP (Lys) #status predicted
F;694,704/Active site: Cys #status predicted
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A;Note: sequence extracted from NCBI backbone (NCBIP:111947)
A;Reference number: A33977; MUID:90046668; PMID:2813355 A;Accession: A33977
                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: S06116; MUID:90032648; PMID:2806244
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'7526-640/Region: actin binding #status predicted
'837-1936/Degion: coiled coil #status predicted <COI>*337-1271/Region: S2
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                                                                                         A; Molecule type: mRNA
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A;Cross-references: UNIPROT:042657; EMBL:AL009227; PIDN:CAA15821.1; GSPDB:GN00066; SPDB:£
A;Experimental source: strain 972h-; cosmid c27D7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1179 AKTHEAQIQEMRÖKHSÖAV----
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Matches 75; Conserv
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NyAlternate names: myosin II

NyAlternate names: myosin II

NyContains: myosin Afrase (EC 3.6.4.1)

CSpecies attus novregicus (Norway rat)

CSpecies attus novregicus (Norway rat)

CACCESSION: S21801; PN0013; $18134

CACCESSION: Chantler, P.D.

J. Mol. Biol. 224, 1185-1193, 1992

A;Title: Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian brain

A;Reference number: S21801; MUID:92235856; PMID:1569576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bpe
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1939 «MER»
A;Cross-references: UNIPROT:Q25662; EMBL:U43145; NID:g1151157; PID:g1151158; PIDN:AACG34
                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Plasmodium chabaudi
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18372
R;Werner, E.B.; Taylor, W.R.; Holder, A.A.
Mol. Biochem. Parasitol. 94, 185-196, 1998
A;Title: A Plasmodium chabaudi protein contains a repetitive region with a predicted
A;Reference number: Z18922; MUID:98418765; PMID:9747969
                                                                                                                                                                              | ::| :| | | | | | | EQLEQTKRVKANLEKA----KQTLENERGELANEVKVILLQGGRDSEHKRKKVBAQLQEL 1257
                ------EELA 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 MKEKNEIIESLDGTINDKKNAYEKLEISFEEKRKMI----EMLDSKLIEKEENFANKQAK 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 IESHHPRLASAVQDHDQIVTSRKSQEPAFHIAGDACLQRKWWV---DVSST-----IYNN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | : :: | : :: | : :: | : :: | TEXENEIIIEKLKDIESREKDFKSKEKF----ASMENELNTLKSDLSKNACQMEVYKL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: | | | | : | | | | | 341 EIXDLSQSLVEXERERIPEIKNEYDDKINNMKEKLSSINDKGIDNTVL--HSEEEKINKLL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 KEKETELNEIHKKYNLEIETIKNEINEKEEELEK------NKKAHTV 439
                                                              EAQRKSKSLKINLNYAGDALRENTLVSEHAQ------RDQRETQCQMKEAEHMYQNE 225
                                                                                                                                                      QDNVNKHTEQQESLDQKLFQLQSKNMMLQQQLVHAHKKADNK-SKITIDIHFLERKMQ-- 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKEKN----AELQMTLKLKESSLTKRASQYSGQLKVLIAENTMLTSKLKEKQDK-EILEAE 114
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                                                                                                                                                                                                                                                                                         1314 QELLQEENROKLSLSTKLK----ÖVEDEK 1338
                                                                                                                                                                                                                                                 283 HHLLKEKNEEIFNYNNHLKNRIYQYEKEK 311
                                                                                                                                                                                                                                                                                                                                                                                                              repeat organellar protein - Plasmodium chabaudi
Query Match
Best Local Similarity 22.5%
Matches 79; Conservative
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A; Molecule type: mRNA
A; Residues: 1-1999 < cstn.>
A; Cross=references: UNIPROT:063731; EMBL:X62659
R; Sun, W.; Chantler, P.D.
Biochem. Biophys. Res. Commun. 175, 244-249, 1991
A; Title: A unique cellular myosin II exhibiting differential expression in the cerebral
A; Reference number: PN0013; MUID:91151356; PMID:1998509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 SLTKRASQYSG------GLKVL-----IAENTMLTSKLKEKQDKEI------LEAE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 IESHHPRLASAVQDHDQIVTSRKSQEPAFHIAGDACLQRKMNVDVSSTIYNNEVLHQPLS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 EAQRK----SKSLKINLNYAGDALRENTLV----SEHAQR----DQRETQCQMKEAEH 220
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38435
R;McDougall, R.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, December 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 LKKEIAMLKLEIATLKHQYQEKENKYFEDIKILKEKNAELQMTLK------LKEE
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22.5%; Pred. No. 0.1;
.ive 55; Mismatches 101; Indels
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A;Accession: T38435
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-750 <MCD>
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A; Map position: 1

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17;
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                                                                                                                       3 TRALOCEVSHTHENENYLLHENCMLXXEIAMLXLEIA-----TLXHQYQEXENXYFED 55
                   68; Gaps
                                                                                                                                                                                                                                    699 GSDDMLIDKEYTRNILFQFLEQRDRRPEIVNLLSILLD-LSEEGKQK 744
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Query Match 10.2%; Score 166; DB 2; Length 750; Best Local Similarity 23.1%; Pred. No. 0.037; Matches 80; Conservative 77; Mismatches 122; Indels
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Search completed: August 1, 2005, 22:23:16 Job time : 22.5308 secs

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1 (Day 1 to 1665)

Yuqiu,J., Dillon,D.C., Mitcham,J.L. and Xu,J.

Yuqiu,J., Dillon,D.C., Mitcham,J.L. and Xu,J.

Compositions for treatment and diagnosis of breast cancer and methods for their use

Patent: US 6518237-A 178 11-FEB-2003;

Location/Qualifiers
AR351137

AR455203

AR4552105

AR28266

AR38266

AR34224

AR34124

AR341424

AR351131

BD271311

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AR345129

AR345400

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/wol_type="genomic DNA"
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Query Match:
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AR280672
LOCUS
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KEYWORDS
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TITLE
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      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Command line parameters:
-MODEL=frame+_p21.model -DEV=Xlp
-MODEL=frame+_p21.model -DEV=Xlp
-G=/GGD1_1/USPTO_spool_p/US09489079/runat_01082005_141250_13297/app_query.fasta_1.1635
-G=/GGD1_1/USPTO_spool_p/US09489079/runat_01082005_141250_13297/app_query.fasta_1.1635
-DEVENTED-10_0FWT=fasta_p -SUFFIX=rge -MINWATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LISS=45
-UNITS=bits -START=1 -END=-1 -MATRIX=100 -TRR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HRAFSIZE=560 -MINLEN=0 -MAXLEN=200000000
-USER=US09489079_@CGN 1 1 8858 @runat_0108205_141250_13297 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGG SCORES=0 -MAIT -DSPBEACK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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AR283168 Sequence
AR341941 Sequence
AR343936 Sequence
                                                                                                     August 1, 2005, 22:24:58; Search time 4799.32 Seconds (without alignments) 3200.517 Million cell updates/sec
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                             nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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AR283168
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Ygapop 10.0 , Ygapext
Pgapop 6.0 , Fgapext
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1: gb_ba: 4

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Unclassified.
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Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L.
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Patent: US 6528054-A 178 04-MAR-2003
Location/Qualifiers
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AR283168 165 bp DN Sequence 178 from patent US 6528054. AR283168.1 GI:29719995

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Hepler,W.T.

Compositions and methods for the therapy and cancer
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Location/Qualifiers
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/mol_type="genomic DNA"
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                       GlutysaksnalagluteuGlnMetThrteuLysLeuLysGluGluSerLeuThrLysArg
                                                                                                  GAAAAGAATGCTGAACTTCAGATGACCCTAAAACTGAAAGAGGAATCATTAACTAAAAGG
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Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and
              LeuHisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThr
                                                    LeutysHisGlnTyrGlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLys
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	AR352903 LOCUS AR352903 LOCUS 100CUS	ψ.	Alignment Scores: 9.68e-116 Length: 1665 Pred. No.: 1632.00 Matches: 317 Score: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 6 Gaps: 0	-09-489-079-25 (1-317) x AR352903 (1-1665) MetGlyThrArgAlaLeuGlnCysGluValSerHisThrHisGluAsnGluAsnTyrLeu	Qy 41 LeulysHisGlnTyrGlnGluLysGluLsnLysTyrPheGluAspIleLysIleLeuLys 60	Qy 81 AlaSerGlnTyrSerGlyGlnLeuLy8ValLeuIleAlaGluAsnThrMetLeuThrSer 100 bb 699 GCATCTCAATATAGTGGGCAGCTTAAAGTTCTGATAGCTGGAACACAATGCTCACTTCT 758 Qy 101 Ly8LeuLy8GluLy8GluAspLy8GluIleLeuGluAlaGluIleGluSerHi8Hi8Pro 120 httl 110 Ly8LeuLy8GluLy8GluIleLeuGluAlaGluIleGluSerHi8Hi8Pro 120 pb 759 AAATTGAAGGAAAACAAGAAATACTAGAGGCAGAAATTGAATCACACCATCCT 818 Qy 121 ArgLeuAlaSerAlaValGlnAspHi8AspGlnIleValThrSerArgLy8SerGlnGlu 140 pb 819 AGACTGGCTTCTGCTGACAAGACCATGATCAAATTGTGACATCAAGAAAAAGTCAAGAA 878 Qy 141 ProAlaPheHi8IleAlaGlyAspAlaCy8LeuGlnArgLy8MetAsnValAspValSer 160 pb 879 CCTGCTTTCCACATTGCTGATGTTTGCAAAGAAAATGAATG

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Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J. and Harlocker,S.L.
Compositions and methods for the therapy and diagnosis of breast
                                                                                                              ProAlaPheHisIleAlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSer
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                                                                                   GCATCTCAATATAGTGGGGCAGCTTAAAGTTCTGATAGCTGAGAACACAATGCTCACTTCT
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	Qy 201 SerGluHisAlaGlnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHis 220	Db 1119 ÅTGTATCAAAACGAACAAGATAATGTGAACAAACACTGAACAGCAGGAGTCTCTAGAT 1178 Qy 241 GlnLysLeuPheGlnLeuGlnSerLysAsnmetTrpLeuGlnGlnGlnLeuValHisAla 260 Db 1179 CAGAAATTATTCAACTACAAAGCAAAATATGTGGCTTCAACAGCAATTAGTTCATGCA 1238	Qy 261 HisLysLysalaAspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLys 280 Db 1239 CATAAGAAAGCTGACAAAAAGCAAGATAACAATTGATTTCTTGAGAGGAAA 1298	Oy 281 MetGlnHisHisLeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeu 300	Oy 301 LysarnargiledyrGlnflyrGluLysgluLysalaGluThrGluAsnSer 317	RESULT 10 AX302858 LOCUS LOCUS DEFINITION Sequence 178 from Patent W00179286. ACCESSION AX302858 VERSION AX302858.1 GI:17383358	Homo sapiens (human) SM Homo sapiens		Unitary, I. T.	CORIXA CORPORATION (US) LOCATION/QUALIFI Ce 1. 1662	/Ab_xref="taxon:9606" ORIGIN	9.68e-116 Length: 1632.00 Matches: 100.00% Conservative:	Best Local Similarity: 100.00* Mismatches: 0 Query Match: 100.00* Indels: 0 DB: 6 Gaps: 0	US-09-489-079-25 (1-317) x AX302858 (1-1665) Qy	Db 459 AIGGGACAGAGCTCTGCAGTTTTTTCTCACACTCAGAAATGAAAATTATCTC 518 Qy 21 LeuHisGluAsnCysMetLeuLystysGlu1leAlaMetLeuLysteuLysteuLystalaThr 40 Dh 519 TTACATGAAAATGAGGAAAAAGGAAATTGCCAAAAAGGGAAAATGCCAACA 578	11 ACALGARMAT IGCALGT TGRAMAGGARMAT IGCCATOCTARMACTGGGARMAT GCCATOCTARMACTGGGARMAT IGCCATOCTARMACTGGGARMAT IGCCATOCTARMACTGGGARMAT IGCCATOCTARMACTGGGARMAT IGCCATOCTARMACTGGGARMAT IGCCATOCTARMACTGGGARMAT IGCCATOCTARMACTGGGARMAT IGCCATOCTARMACTGGARMAT IGCCATOCTARMACTGGARMAT IGCCATOCTARMACTGGARMAT IGCCATOCTARMACTGGARMAT IGCCATOCTARMACTGGARMAT IGCCATOCTARMACTGGARMAT IGCCATOCTARMACTGARMAT IGCCATOCTARMACTGARMACTGGARMAT IGCCATOCTARMACTGARMACTARMACTGARMACTARMACTGARMACTGARMACTARMACTGARMACTARMACTGARMACTARMACTGARMACTARMACTGARMACTARMACTGARMACTARMACTGARMACTGARMACTARMACTGARMACTARMACTGARMACTARMACTGARMACTARMACTGARMACTARMACTGARMACTARMACTARMACTARMACTGARMACTA
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Qy 12 Db 81	ч 6		
Oy 14 Db 87	41 ProAlaPheHisIleAlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSer 160 		
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DEFINITION ACCESSION VERSION	Sequence 468 from patent US 6528054. AR283456 AR283456.1 GI:29720283	Qy 2	221 MeciyrGinasnGluGli
ΣS	Unknown. Unknown.		241 GlnLysLeuPheGlnLe
REFERENCE AUTHORS	Unclassilled 2. 1 (bases 1 to 2.307) Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and	o vo	
TITLE	Hepler, W.T. Compositions and methods for the therapy and diagnosis of breast cancer. Patent: US 6528054-A 468 04-MAR-2003;	ob 18	1846 CATAAGAAAGCTGACAA 281 MetGlnHisHisLeuLe

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        21 LeuhisGluasnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThr
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1 (Dasses 1 to 2307)

Jiang, Y., Dillon, D.C., Mitcham, J.L., Xu, J., Harlocker, S.L. and Hepler, W.T.
                                                          SerGluHisAlaGlnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHis
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468 from patent US 6586572.
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                                                                                                                                                                                 Unknown.
Unclassified.
I (bases I to 2307)
Yugiu,J., Dillon,D.C., Mitcham,J.L., Xu,J. and Harlocker,S.L.
Compositions for the treatment and diagnosis of breast cancer and methods for their use
methods for their use
Patent: US 6579973-A 468 17-JUN-2003;
Location/Qualifiers
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AUTHORS	I (Dases I to 2307) Jiang,Y., Dillon,D.C., Mitcham,J.L., Xu,J., Harlocker,S.L., Hanler W. T. and Handeren D. A.	Qy 261 Histy	-3-
TITLE	Compositions and methods for the therapy and diagnosis of breast cancer	Db 1846 CATAA	-5
JOURNAL FEATURES	Patent: US 6680197-A 468 20-JAN-2004; Location/Qualifiers	281	ᇊ
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GenCore version 5.1.6
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- protein search, using sw model OM protein

Run on:

August 1, 2005, 22:04:01; Search time 112.678 Seconds (without alignments) 1088.086 Million cell updates/sec

US-09-489-079-25

Title: Perfect score:

1632 1 MGTRALQCEVSHTHENENYL......NHLKORLIYQYEKEKAETENS 317 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aab07639 Amino aci	Aab50261 Human bre	0 B726P	Human	Human	Abg78910 Human bre	Human	Human	Human	Aau33353 Human pro	Abg78920 Human bre	Human	Human 1	Human		Abj37749 Human tum	Adl93157 Human bre	Abj37781 Human tum	Human		B726P	Human	Human	Abg78912 Human bre	Abj37735 Human tum
ID	AAB07639	AAB50261	AAG65980	AAU33343	AA015777	ABG78910	ABJ37733	ADL92838	ADE44128	AAU33353	ABG78920	ABJ37743	ADL93145	AAU33359	ABG78926	ABJ37749	ADL93157	ABJ37781	ADL93213	AAB50244	AAG65982	AAU33345	AA015779	ABG78912	ABJ37735
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Length	317	317	317	317	317	317	317	317	317	323	323	323	323	410	410	410	410	324	324	432	432	432	432	432	432
% Query Match	100.0	99.4	99.4	99.4		99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.1	99.1	97.2	97.2	97.2	97.2	97.2	97.2
Score	1632	1622	1622	1622	1622	1622	1622	1622	1622	1622	1622	1622	1622	1622	1622	1622	1622	1617	1617	1586	1586	1586	1586	1586	1586
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-	Human	Human	Abg78918 Human bre	Human	Amino	_	Abj37784 Human tum	Breast	Adl93227 Human bre	Abj37783 Human tum	Human 1	Human	Ad193235 Human bre						
ADL92843	ADE44133	AAU33351	ABG78918	ABJ37741	ADL93137	ADE44427	AAU33357	ABG78924	ABJ37747	ADL93155	AAB84702	ABJ05537	ABJ37784	ABR47548	ADL93227	ABJ37783	ADL93215	ABJ37788	ADL93235
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97.2	97.2	97.2	97.2	97.2	97.2	97.2	97.2	97.2	97.2	97.2	97.2	97.2	97.2	97.2	97.2	9.96	96.6	96.6	9.96
1586	1586	1586	1586	1586	1586	1586	1586	1586	1586	1586	1586	1586	1586	1586	1586	1576	1576	1576	1576
56	27	28	5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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BS322; breast tissue marker; breast disease; breast cancer.
                                                                                                                                                                       Amino acid sequence of BS322 polypeptide.
                                        AAB07639 standard; protein; 317 AA.
                                                                                                                                (first entry)
                                                                                                                                07-NOV-2000
                                                                                   AAB07639;
RESULT 1
                      AAB07639
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WO200043420-A1. Homo sapiens. 27-JUL-2000.

21-JAN-2000; 2000WO-US001452.

99US-00234716. (ABBO) ABBOTT LAB 21-JAN-1999;

Cohen M, Colpitts TL, Friedman PN, Gordon J; es SC, Klass MR, Kratochvil JD, Russell JC; Billing-Medel PA, Cohen | Granados EN, Hodges SC, Stroupe SD;

WPI; 2000-499217/44. N-PSDB; AAA59015.

BS322-specific polynucleotides, polypeptides and antibodies, used in the detection and diagnosis of breast disease especially breast cancer.

Claim 23; Page 123-124; 126pp; English.

The present sequence represents a human BS322 polypeptide. BS322 is a breast tissue marker. The BS322 polynucleotides and polypeptides are used to detect and disgnose breast disease, e.g. breast cancer. The BS322 polynucleotides are useful as a source of probes and primers, and the BS322 polypeptides are useful as antigens

Sequence 317 AA;

ö Gaps ö Query Match 100.0%; Score 1632; DB 3; Length 317; Best Local Similarity 100.0%; Pred. No. 5.7e-118; Matches 317; Conservative 0; Mismatches 0; Indels 0; ~

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                                                                                                               MGTRALQCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILK
                                                 EKNAELQMTLKLKEESLTKRASQYSGQLKVLIAENTMLTSKLKEKQDKEILEAEIESHHP
                                                                 EKNAELQMTLKLKEESLTKRASQYSGQLKVLIAENTWLTSKLKEKQDKEILEAEIESHHP
                                                                                                   121 RLASAVQDHDQIVTSRKSQEPAFHIAGDACLQRKMNVDVSSTIYNNEVLHQPLSEAQRKS
                                                                                                                                                   KSLKINLNYAGDALRENTLVSEHAQRDQRETQCQMKEAEHMYQNEQDNVNKHTEQQESLD
                                                                                                                                                                   MGTRALOCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHOYOEKENKYFEDIKILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the coding sequences and some protein sequences of proteins associated with breast cancer in humans. These sequences can be used in the diagnosis and treatment of cancers, particularly breast tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; breast cancer associated gene; vaccine; diagnosis; therapy.
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                                                                                                                                                                                                                                                                                                                                                AAB50261 standard; protein; 317
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99US-00339338.
99US-00389681.
99US-00433826.
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tumor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to identifying tissue-specific polymucleotides (First involves performing a genetic subtraction to identify pool of (P) from tissue of interest (TI), performing DNA microarray analysis to identify first subset of polymucleotides (SP1) at least 2-fold over expressed in TI, and sperforming quantitative polymerase chain reaction (PCR) analysis on SP1 to identify second subset of (P). The method is useful for determining the presence or absence of a cancer cell in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying tissue (tumor)-specific polynucleotides overexpressed in tissue of interest as compared to control tissue, for detecting cancer cells in patient, comprises DNA microarray analysis or quantitative polymerase chain reaction.
                 MGTRALQCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILK
                                                     EKNABLIQMTLKLKBESLTKRASQYSGQLKVLIAENTWLTSKLKEKQDKEILEAEIESHHP
                                                                          EKNAELQMTLKLKEESLTKRASQYSGQLKVLIAENTWLTSKLKEKQDKEILEAEIESHHP
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 MGTRALQCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILK
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2000US-0219862P.
2000US-0221300P.
2000US-0256592P.
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20-JUL-2000;
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18-DEC-2000;
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                                                                                                                                                                                                                                                                                                      patient, monitoring the progression of cancer in a patient using a blological sample such as blood, serum, lymb nodes, bone marrow, sputum, urine or a tumour biopsy sample. The methods are useful for determining the presence or absence of or monitoring progression of prostate, breast, colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver, gastric, kidney, bladder, pancreatic or endometrial cancer. The present sequence represents the B726F first splice variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; breast cancer protein; tumour; cancer; cytostatic;
                                                                                              99.4%; Score 1622; DB 4; Length 317;
100.0%; Pred. No. 3.4e-117;
tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human breast cancer protein encoded by cDNA cloneB726P-20
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                                                                                                                                                                                                                                                                                                                                                                                                      AAU33343 standard; protein; 317
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08-JUN-2000; 2000US-00590751.
22-JUN-2000; 2000US-00604287.
20-JUL-2000; 2000US-00620405.
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                                                                                                                  Matches 315; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-611721/70.
N-PSDB; AAS47120.
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                                                                                                         Local Similarity
                                                                             Sequence 317 AA;
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The invention relates to isolated breast tumour proteins and nucleic acids that encode them, including immunogenic fragments of the proteins. Also included are expression vectors expressing the proteins, transfoormed cells and antibodies raised against the proteins or an antigen presenting cell expressing the protein. The proteins or an antigen presenting call expression, diagnosis and treatment of diseases associated with imappropriate breast tumour protein expression, i.e. breast tumours and breast cancer e.g by gene therapy. The nucleic acids and their complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in necleic acids in samples, and therefore which patients may be in necleic acids in samples, modulators (e.g. antagonists) of breast tumour protein expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down cell and protein expression and activity. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down cell and activity in the antibodies may also be used to down regulate expression and activity. The antibodies may also be used to down cell and activity from a present sequence is a breast tumour protein encoded by a cDNA from a breast tumour cDNA library isolated by subtractive hybridisation against a normal breast cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 EKNAELOMTLKLKEESLTKRASQYSGQLKVLIAENTWLTSKLKEKQDKEILEAEIESHHP 120
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100.0%; Pred. No. s...
0; Mismatches
diagnosis and treatment of breast cancer.
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                                                                        Claim 3; Page 197; 297pp; English
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hes 315; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 317 AA;
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JS2002085998-A1
        Human; breast
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23-JUN-1999;
02-SEP-1999;
03-NOV-1999;
                            Homo sapiens
                                                                   04-JUL-2002
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                                                                                                                                                                                                                                     The invention comprises a protein which contains an immunogenic portion of a breast antigen. The invention also comprises breast antigen-related DNA sequences. The protein of the invention is useful as a vaccine for inhibiting the development of breast cancer. The protein of the invention is used in adoptive immunotherapy for the treatment of cancer, and a perient. The present amino acid sequence represents a duministered to a patient. The present amino acid sequence represents a human breast antigen protein of the invention
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                                                                                                                                                                            Novel isolated polypeptide comprising an immunogenic portion of a breast antigen, useful for treating breast cancer or for inhibiting the development of breast cancer in a patient.
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100.0%; Pred. No. 3.4e-117;
tive 0; Mismatches 0; Indels
                                                                                                                             Xu J;
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                                                                                                                             Mitcham JL,
                                                                                                                                                                                                                     Claim 2; Page 77; 127pp; English
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                                              98US-00222575.
                            99US-00339338
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Best Local Similarity 100.(
Matches 315; Conservative
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                                                                           YUQIU J.
DILLON D C.
MITCHAM J L.
                                                                                                                            Yugiu J, Dillon DC,
                                                                                                                                               WPI; 2002-697821/75.
                                                                                                                                                          N-PSDB; ABT08775
                                                                                                                                                                                                                                                                                                                               Sequence 317 AA;
                                                                                                          XU J.
                                                          02-APR-1999;
                            23-JUN-1999;
                                               38-DEC-1998;
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        01-AUG-2002
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The invention relates to an isolated breast tumour polynuclectide and the polypeptide it encodes. The polynuclectide and polypeptide are useful for phetecting the presence of breast cancer in a patient, and in pharmaceutical compositions for treating breast cancer. The sequences are useful for stimulating an immune response in a patient and can therefore detecting in production of vaccines. The sequences are also useful for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with a composition of the invention and detecting the amount of polynucleotide that hybridizes to the sample. This sequence represents a human breast tumour polypeptide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel breast cancer polynucleotides and polypeptides encoded by the polynucleotides, useful for detecting the presence of breast cancer in a patient, and in pharmaceutical compositions, for treating breast cancer.
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protein; breast cancer; cytostatic; vaccine
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Best Local Similarity 100.0%; Pred. No. 3.4e-117;
Matches 315; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 106-107; 247pp; English.
                                                                                                                                                                                                                                                                                                                                                98US-0022575.
99US-00285480.
99US-00339338.
99US-00389681.
99US-00433826.
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08-JUN-2000; 2000US-00590751.
08-JUN-2000; 2000US-00604287
20-JUL-2000; 2000US-00620405
                                                                                                                                                                                                                                                                                   13-APR-2001; 2001US-00834759
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Henderson RA;
          tumour
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241 QKLFQLQSKNMMLQQQLVHAHKKADNKSKITIDIHFLERKMQHHLLKEKNEEIFNYNNHL 300
181 KSLKINLNYAGDALRENTLVSEHAQRDQRETQCQMKEAEHMYQNEQDNVNKHTEQQESLD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated breast cancer-associated polypeptide. The polypeptide may be used for the diagnosis and treatment of breast cancers. The methods are useful for detecting the presence of scancer in a patient and treating a cancer in a patient. The present sequence represents the amino acid sequence of a human breast cancer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An isolated oncogenic polypeptide useful for preventing, diagnosing and treating breast cancer.
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                              OKL FOLOSKNIMILOOOLVHAHKKADINKSKITIDIHFLERKMOHHLLKEKNEEIFIVYNINHL
                                                                                                                                                                                                                                                                                                              gene therapy; protein therapy; vaccine; breast cancer; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 317;
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                                                                                                                                                                                                                                                                                   Human breast cancer-associated polypeptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 176; 294pp; English.
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                                                                                                                                                                                               ADL92838 standard; protein; 317 AA
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99US-00285480.
99US-0039338.
99US-00389681.
99US-00433826.
2000US-00551621.
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2000US-00620405.
2001US-00834759.
2001US-00007805.
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                                                                                         KORIYQYEKEKAETE 315
                                                                                                                                                                                                                                                         (first entry)
                                                                                                          301 KNRIYQYEKEKAETE
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Best Local Similarity 100.
Matches 315; Conservative
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08-JUN-2000;
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23-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLASAVQDHDQIVTSRKSQEPAFHIAGDACLQRKMNVDVSSTIYNNEVLHQPLSEAQRKS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSLKINLNYAGDALRENTLVSEHAQRDQRETQCQMKEAEHMYQNEQDNVNKHTEQQESLD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises a method of stimulating and/or expanding T cells specific for a tumour protein. The invention further comprises human nucleic acids and proteins that are associated with tumours (e.g. breast cancer). The method and sequences of the invention are useful for stimulating and/or expanding T cells specific for a tumour protein, detecting the presence of cancer, stimulating an immune response in a patient and treating breast cancer. The present amino acid sequence represents a human tumour-related protein
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                                                                                                                                                                                                                             expansion;
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Hepler WT, Henderson RA,
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                                                                                                                                                                                                                                             tumour; breast cancer; cancer; immune response stimulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 99.4%; Score 1622; DB 6; Length 3 Local Similarity 100.0%; Pred. No. 3.4e-117; les 315; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                             Human; vaccine; gene therapy; T cell stimulation; T cell
                                                                                                                                                                                               Human tumour-related protein - SEQ ID No 176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 207-208; 375pp; English
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Mcneill PD, Durham M;
                                                                                                          ABJ37733 standard; protein; 317 AA
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07-DEC-2001; 2001US-00007805.
13-FEB-2002; 2002US-00076622.
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       KNRIYQYEKEKAETE 315
                                KNRIYOYEKEKAETE 315
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Vedvick TS,
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                                                        Sequence 317 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated polypeptide comprising at least an immunogenic portion of a breast tumour protein. The polymuclectide, its pulyapetide, its antibody, a pharmaceutical composition comprising the fusion protein or the polymuclectide encoding it, a vaccine comprising the fusion protein or the polymuclectide encoding it, an isolated T cell population comprising T cells specific for a breast tumour protein, and a method for removing tumour cells from a biological sample is useful for inhibiting the development of a cancer in a patient. The polypeptide is
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inhibiting
        RLASAVQDHDQIVTSRKSQEPAFHIAGDACLQRKMNVDVSSTIYNNEVLHQPLSEAQRKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated polypeptide comprising immunogenic portion of protein or its variant, useful for formulating vaccines for cancer development in a patient.
                                                                                                                                                                                                                                                                tumour; cancer; vaccine; T cell stimulator;
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                                                                                                                                                                                            ADE44128 standard; protein; 317 AA
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99US-00285480.
99US-00339338.
99US-00389681.
99US-00433826.
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DILLON D C.
MITCHAM J L.
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expander.
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23-JUN-1999;
02-SEP-1999;
03-NOV-1999;
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T cell
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useful for stimulating and/or expanding T cells specific for a breast tumour protein. Stimulating and/or expanding T cells specific for a breast tumour protein is useful for inhibiting the development of a cancer in a patient. The method additionally involves the step of cloning at least one proliferated cell and then administering the cloned T cells to the patient. The present sequence represents a breast cancer protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKNAELOMTLKLKEESLTKRASQYSGQLKVLIAENTWLTSKLKEKODKEILEAEIESHHP 120
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                                                                                                                                                                                                                                                                     99.4%; Score 1622; DB 8; L. Local Similarity 100.0%; Pred. No. 3.4e-117; les 315; Conservative 0; Mismatches 0;
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08-JUN-2000; 2000US-0059751.
22-JUN-2000; 2000US-006204287.
20-JUL-2000; 2000US-00620405.
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gene therapy; immunogen
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2001US-00834759

13-APR-2001;

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28-DEC-1998; 98US-0022575.
02-APR-1999; 99US-00286480.
23-UUN-1999; 99US-00339338.
02-SEP-1999; 99US-00339338.
03-MOV-1999; 99US-00433826.
17-APR-2000; 2000US-00551621.
08-UUN-2000; 2000US-0059751.
acide that encode them, including immunogenic fragments of the proteins. Also included are expression vectors expressing the proteins, transformed cells and antibodies raised against the proteins or an antigen presenting cell expressing the protein. The proteins and nucleic acide may be used in the prevention, diagnosts and treatment of diseases associated with inappropriate breast tumour protein expression, i.e. breast tumours and breast cancer e.g by gene therapy. The nucleic acide and their and quantitate the presence of similar nucleic acide in samples, and therefore which patients may be in need of restorative therapy. The proteins, nucleic acide and antibodies may be used in assays to identify
                                                                                                                                                                                                                                                                                                                            modulators (e.g. antagonists) of breast tumour protein expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immunotaristion diagnostic techniques. The present sequence is a breast tumour protein encoded by a CDNA from a breast tumour cDNA library isolated by subtractive hybridisation against a normal breast CDNA
                                                               The invention relates to isolated breast tumour proteins and nucleic
                       Example 6; Page 286-287; 297pp; English.
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Sequence 323 AA;

Novel breast cancer polynucleotides and polypeptides encoded by the polynucleotides, useful for detecting the presence of breast cancer in a patient, and in pharmaceutical compositions, for treating breast cancer.

Example 7; Page 215-216; 247pp; English

Hepler WT;

Harlocker SL,

Χu J,

Mitcham JL,

Dillon DC,

Henderson

Jiang Y,

WPI; 2002-635657/68. N-PSDB; ABS64018.

20-JUL-2000; 2000US-00620405

(CORI-) CORIXA CORP

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                                                            RLASAVODHDOI VTSRKSQEPAFHIAGDACLQRKMVDVSSTI YNNEVLHQPLSEAQRKS
                                                                                                                                                                                                  KSLKINLNYAGDALRENTLVSEHAQRDQRETQCQMKEAEHMYQNBQDNVNKHTEQQESLD
                                                                                           EKNAELQMTLKLKEESLTKRASQYSGQLKVLIAENTMLTSKLKEKQDKEILEAEIESHHP
                                                                                                                                        RLASAVQDHDQIVTSRKSQEPAFHIAGDACLQRKMNVDVSSTIYNNEVLHQPLSEAQRKS
                                                                                                                                                                                    KSLKINLNYAGDALRENTLVSEHAQRDQRETQCQMKEAEHMYQNEQDNVNKHTEQQESLD
                                               MCTRALQCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILK
                           Gaps
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99.4%; Score 1622; DB 4; Length 323; 100.0%; Pred. No. 3.5e-117; tive 0; Mismatches 0; Indels
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                           Matches 315; Conservative
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The invention relates to an isolated breast tumour polynucleotide and the polypeptide it encodes. The polynucleotide and polypeptide are useful for detecting the presence of breast cancer in a patient, and in pharmaceutical compositions for treating breast cancer. The sequences are useful for stimulating an immune response in a patient and can therefore be used in production of vaccines. The sequences are also useful for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with a composition of the invention and detecting the amount of polynucleotide that hybridizes to the sample. This sequence represents a human breast tumour polypeptide of the invention
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                                                                                                                                                                                                                                                                                                                                           99.4%; Score 1622; DB 5; L 100.0%; Pred. No. 3.5e-117; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                  Sequence 323 AA;
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ABJ37743 standard; protein; 323 AA. RESULT 12 ABJ37743 ID ABJ3

Human; breast tumour protein; breast cancer; cytostatic; vaccine.

US2002085998-A1 Homo sapiens

04-JUL-2002

Human breast tumour polypeptide #12

15-NOV-2002 (first entry)

ABG78920 standard; protein; 323 AA.

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301 KNRIYOYEKEKAETE 315
                                           ADL93145
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                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises a method of stimulating and/or expanding T cells specific for a tumour protein. The invention further comprises human nucleic acids and proteins that are associated with tumours (e.g. breast cancer). The method and sequences of the invention are useful for stimulating and/or expanding T cells specific for a tumour protein, patient and treating breast cancer. The present amino acid sequence represents a human tumour-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 EKNAELÓMTLKLKEESLTKRASÓYSGOLKVLIAENTMLTSKLKEKODKEILEAEIESHHP 120
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                                                                                                                                                                                                                                                             Dillon DC;
Henderson RA, Fanger GR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                        Human, vaccine, gene therapy, T cell stimulation, T cell expansion, tumour; breast cancer, cancer; immune response stimulation.
                                                                                                                                                                                                                                                                                                                              New polypeptide and polynucleotide useful for stimulating and/or expanding T cells specific for a tumor protein and treating breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.4%; Score 1622; DB 6; Length 323; 100.0%; Pred. No. 3.5e-117; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                             Sleath PR, Persing DH, Jiang Y,
Xu J, Harlocker SL, Hepler WT, H
Mcneill PD, Durham M;
                                                    Juman tumour-related protein - SEQ ID No 483.
                                                                                                                                                                                                                                                                                                                                                                         Example 7; Page 303-304; 375pp; English.
                                                                                                                                                                                             13-APR-2001; 2001US-00834759.
07-DEC-2001; 2001US-00007805.
13-FEB-2002; 2002US-00076622.
                                                                                                                                                                        15-APR-2002; 2002WO-US012378.
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                              (first entry)
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Best Local Similarity 100.
Matches 315; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 323 AA;
                                                                                                                              WO200283956-A1.
                                                                                                           sapiens
                                                                                                                                                                                                                                                               Houghton RL,
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Vedvick TS,
                              15-MAY-2003
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          ABJ37743;
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61 BKNAELQWTLKLKEESLTKRASQYSGQLKVLIAENTWLTSKLKEKQDKEILEAEIESHHP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated breast cancer-associated polypeptide. The polypeptide may be used for the diagnosis and treatment of breast cancers. The methods are useful for detecting the presence of cancer in a patient and treating a cancer in a patient. The present sequence represents the amino acid sequence of a human breast cancer-associated polypeptide.
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                                                                                                                                                                            gene therapy; protein therapy; vaccine; breast cancer; cancer; human.
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                                                                                                                                    Human breast cancer-associated polypeptide #12
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Ä.
ADL93145 standard; protein; 323
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2000US-00590751.
2000US-00604287.
2000US-00620405.
2000US-00834759.
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99US-00285480.
99US-00339338.
99US-00389681.
99US-00433826.
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                                                                                       (first entry)
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Matches 315; Conservative
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02-SEP-1999;
03-NOV-1999;
17-APR-2000;
26-JUN-2000;
20-JUL-2000;
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07-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houghton RL,
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                                                                                       20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-1998
                                                                                                                                                                                                                                                                                                                      04-SEP-2003
                                             ADL93145;
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Sequence 410 AA;

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The invention relates to isolated breast tumour proteins and nucleic acids that encode them, including immunogenic fragments of the proteins. Also included are expression vectors expressing the proteins, transformed cells and antibodies raised against the proteins or an antigan presenting cell expressing the protein and antibodies raised against the proteins and anticapen presenting cell expressing the protein. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate breast tumour protein expression, i.e. breast tumours and breast cancer e.g by gene therapy. The nucleic acids and their complements may also be used as DMA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and quantitate the presence of similar nucleic acids in samples, and confidence with a nucleic acids and antibodies may be used in assays to identify modulators (e.g. antagonists) of breast tumour protein expression and activity. The antibodies mad antibodies may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)) and in other immunocorpus tumour protein encoded by a cDNA trom a breast tumour cDNA library library
                             KSLKINLNYAGDALRENTLVSEHAQRDQRETQCQMKEAEHMYQNEQDNVNKHTEQQESLD 240
                                                                                           QKLFQLQSKNMWLQQQLVHAHKKADNKSKITIDIHFLERKWQHHLLKEKNEEIFNYNNHL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Breast Tumor Proteins and nucleic acids useful for the prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; 88; breast cancer protein; tumour; cancer; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 24; Page 296-297; 297pp; English.
                                                                                                                                                                                                                                                                                                                                                          AAU33359 standard; protein; 410 AA
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08-JUN-2000; 2000US-00590751.
22-JUN-2000; 2000US-00604287.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy; immunogen
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                                                                                                                                                                                                                                               QKLPQLQSKNMWLQQQLVHAHKKADNKSKITIDIHFLERKMQHHLLKEKNEEIFNYNNHL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel breast cancer polynucleotides and polypeptides encoded by the polynucleotides, useful for detecting the presence of breast cancer in a patient, and in pharmaceutical compositions, for treating breast cancer.
                                                    9
                                                                                                                       154 EKNAELOMTLKLKEESLITKRASOYSGOLKVLIAENTMLTSKLKEKODKEILEAEIESHHP
                                                                                                                                                              KSLKINLNYAGDALRENTLVSEHAQRDQRETQCQMKEAEHMYQNEQDNVNKHTEQQESLD
                                                   1 MGTRALQCEVSHTHENENYLLHENCMLKKEIAMLKLEIATLKHQYQEKENKYFEDIKILK
                                                                                                   61 BKNAELQMTLKLKEESLTKRASQYSGQLKVLIAENTMLTSKLKEKQDKEILEAEIESHHP
                                                                                                                                                  121 RLASAVQDHDQIVTSRKSQEPAFHIAGDACLQRKMNVDVSSTIYNNEVLHQPLSEAQRKS
                            Gaps
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      Length 410;
                            0; Indels
      Score 1622; DB 4; I
Pred. No. 4.7e-117;
99.4%; Score 100.0%; Pred. No. 4.7e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human breast tumour polypeptide #17.
                                                                                                                                                                                                                                                                                                                                                                                   ABG78926 standard; protein; 410 AA.
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99US-00339338.
99US-00389681.
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2000US-00551621.
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22-JUN-2000;
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Hepler WT;

Harlocker SL,

Disclosure; Page 228-229; 247pp; English.

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The invention relates to an isolated breast tumour polynucleotide and the polypeptide it encodes. The polynucleotide and polypeptide are useful for detecting the presence of breast cancer in a patient, and in pharmaccutical compositions for treating breast cancer. The sequences are useful for stimulating an immune response in a patient and can therefore be used in production of vaccines. The sequences are also useful for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with that hybridizes to the sample. This sequence represents a human breast tumour polypeptide of the invention
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Sequence 410 AA;

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                                                                                       EKNAELQMTLKLKEESLTKRASQYSGQLKVLIAENTMLTSKLKEKQDKETLEAETESHHP
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-BT0534-281299-053-a01&t2=11999-12-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 565.
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1. (bases 1 to 565)

HCGP http://www.ludwig.org.br/ORESTES.

The FARESP/LICR Human Cancer Genome Project
Unpublished (1999)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Copyright (c) 1993 - 2005 Compugen Ltd.
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//octe="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and so circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
                                L. Jackes L. C. 222. A Radelof, L. Beill, O. Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B. Human Unigeneset - RZPD3

AL Unpublished (2003)

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD1.B; IMAGP9981196637.

RZPD1.B; IMAGP9981196637.

RZPD1.B; I.M.A.G.E. CDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/Cgi-
hin/showlib.pl.cgi/response71ibNo-872 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 111

www.rzpd.de
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 AlaGlnArgLysSerLysSerLeulysIleAsnLeuAsnTyrAlaGlyAspAlaLeuArg 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 CAGGAGTCTCTAGATCAGAAATTATTTCAACTACAAAGCAAAAATATGTGGCTTCAACA 302
                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free from RZPD; contact RZPD; contact RZPD (clone@rzpd.de) for further information. Seg primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GCTCAAAGGAAATCCAAAAGCCTAAAAATTAATCTCAATTATGCAGGAGATGCTCTAAGA
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malia; Butheria; Primates; Catarrhini; Hominidae; Homo
(bases 1 to 492)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .492
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGP9981196637 ; IMAGE:2659290"
/lab_host="DH108"
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/db_xref="taxon:9606"
|de_stage="Adult" |
|/de_stage="Adult" |
|/clone lib="Br034" |
|/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
|/main; Amin-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 GTACAAGACCATGATCAAATTGTGACATCAAGAAAAAGTCAAGAACCTGCTTTCCACATT 420
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 caagacaaagaaaracragagggagaaarrgaarcacaccarccragacrggcrrcrgcr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 AATGAGGTGCTCCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCAAAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuGlnCysGluValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys
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BX282243 Soares NFL T GBC S1 Homo sapiens CDNA clone IMAGP9981196637; IMAGE:2659290, mRNA sequence.
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Matches:
Conservative:
Mismatches:
Indels:
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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CK749347 4760 bp mRNA linear HTC 19-AUG-2004
Homo sapiens mRNA; cDNA DKFZp781D1722 (from clone DKFZp781D1722).
CR749347
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the
Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZP)81D1722) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contect RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp781D1722
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 GAAATACTGGAGACAGAAATTGAATCACCATCCTAGACTGGCTTCTGCTTTACAAGAC 153
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1 (bases 1 to 4760)
2 (bases 1, to 4760)
3 (bases 1, to 4760)
4 (bases 1, to 4760)
5 (bobo,G., Han,M. and Wiemann,S.)
7 (base 1, Han,M. and Wiemann,S.)
7 (base 2 (base 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 GCTCCTTTGCAAGGAATAATGAATGTTGATGTGAATACATA-TATAACAT-GAGGTG 35
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                                                                                                                                                                                                                                                                       GluValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLys
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Homo sapiens
   647.50
87.65%
80.59%
39.68%
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Best Local Similarity:
Query Match:
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1 (bases 1 to 650)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpsonedidwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=RCI-HT0598-140 300-021-b02&t3=2000-03-14&t4=1)
Seq primer: puc 18 forward High quality sequence start: 24 High quality sequence stop: 569.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE177744 650 bp mRNA linear EST 22-JUN-2000
RC1-HT0598-140300-021-b02 HT0598 Homo sapiens CDNA, mRNA sequence.
BE177744
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                                                                                                                                                                                                                                                                                                                                                                         423 TACAATAACCATTTAAAAAACCGTATATATCAATATGAAAAAGAGAAAGCAGAAACAGAA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                TyrAsnAsnHisLeuLysAsnArgIleTyrGlnTyrGluLysGluLysAlaGluThrGlu
                                             GlnLeuValHisAlaHisLysLysAlaAspAsnLysSerLysIleThrIleAspIleHis
                                                                                                                                                                        PheleuGluarglysMetGlnHisHisLeuLeuLysGluLysAsnGluGluIlePheAsn
                                                                                                                                                                                                                                       TTTCTTGAGAGAAAATGCAACATCATCTCCTAAAAAGAGAAAAATGAGAGATATTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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/dev_stage="Adult"
/clone_lib="HT0598"
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MEDLINE PUBMED COMMENT

JOURNAL

TITLE

650

Length:

9.01e-59

Alignment { Pred. No.:

Bource

FEATURES

168

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HSM801761 3527 bp mRNA linear HTC 22-SEP-2004
Homo sapiens mRNA; cDNA DKFZp434A171 (from clone DKFZp434A171).
AL136793
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                                                                                                                                                               237
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                                                                                                                                                                                                                                                                                                                        274
                                                                                                                                                                                                                                            257
                                                                                                                                                                                                                                                                                                                                                                Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s. wiemann@dkfz-heidelberg.de;
sequenced by DKPZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZP434A171) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp434A171
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
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Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Well,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/clone_lib="434 (synonym: htes3). Vector pSportl; host
DH108; sites NotI + SalI"
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                                                                                                     218 AlaGluHisMetTyrGlnAsnGluGlnAspAsnValAsnLysHisThrGluGlnGlnGlu
                                                                                                                                                                                      747 ATTGAACAAATGTTTCAGAATGAAGAAGACAAAGTGAGTAAATACATTCAAAAAGCAAGAA
                                                                                                                                                                                                                                            SerieuAspGlnLysLeuPheGlnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeu
                                                                                                                                                                                                                                                                                                                        258 ValHisAlaHisLysLysAlaAspAsnLysSerLysIleThrIleAspIle------
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Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
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                                                                                                                    /tissue_type="testis"
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DH10B; sites alla + SfilB"
/dev_stage="adult"
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LKNKWHQTROALKEKTLVLEDVQRDLTQSQCRRKEIEQMFQNBEDKVSKYIQKQESLE
BRLSQIQNBNLLLRQQLDEAYKKADNQEETIINIQEQFNAIVKNQAGSEBGSLLLEQK
NNNLINKCDFIKKKIV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAla 125
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65
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25
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                      product="hypothetical protein"
protein id="CAH18200.1"
db_xref="G1:51476420"
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                                                                                                                                                                                                                                          gene="DKFZp781D1722"
    location/Qualifiers
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647.00
65.03$
45.09$
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Query Match:
DB:
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 63 Row: e Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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CA 94305
2276
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2457 AGTAAGAAGCTAATGAATGAATGATCATTTAAAAGAAAGTCTCTTTCAGTATGAGAGA 2516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC help desk
Email: cgapbs.remail.nih.gov
Tissue Prcourement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shirak:
Toshiyuki and Piero Carninci (RIKEN)
TOShiyuki and Piero Carninci (RIKEN)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 9431
Web site:
http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.
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Submitted (31-701-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                             231 LysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnSerLysAsn
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                                                                                 ThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspAsnValAsn
                                                                                                                                                                                                                                                                                                                            251 MetTrpleuGlnGlnGlnLeuValHisAlaHisLysLysAlaAspAsnLysSerLysIle
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Catarrhini; Hominidae; Homo.
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mRNA.
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Homo sapiens, clone IMAGE:5265638,
BC036210
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5265638"
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Homo sapiens
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ALDKDNNTPLLFAIICKKKKMVEFLLKKKASSHAVDRLRRSALMLAVYYDSPGIVNIL
LKQNIDVFAQDMCGRDAEDYAISHHLTKIQQQILEHKKKILKKEKSDVGSSDESAVSI
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                                                                                                                                                                                                                                           /db_xref="UniProt/TrEMBL:Q9H0H6"
/translation="MKLFGFGSRRGQTAQGSIDHVYTGSGYRIRDSELQKIHRAAVKG
DAAEVERCLARRSGDLDALDKQHRTALHLACASGHVQVVTLLVNRKCQIDVCDKENRT
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2037 GTACAAGTAGAGTICTGCTATTICCAAAGTAAAAGCTGAGAATGAGTITCTACT
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Mismatches:
Indels:
                                                                                                                          /codon_start=1
/product="hypothetical protein"
/protein_id="CAB66727_1"
/db_xref="GI:12053099"
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Matches:
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/gene="DKFZp434A171"
                                  gene="DKFZp434A171"
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University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@niowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CONA Library Preparation: N. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com)
Seq primer: M13 FORWARD
POLYA=Yes.
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2792 GAGAAAATCAGACATTAATCAACGAATGCAATCATTTTTTAAAAGGCTTCAACAACAG 2851
      GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsnArgIleTyrGlnTyr 307
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Normalization and subtraction: two approaches to facilitate gene
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TAG_LIB=UT-CF-DUI
TAG_SEQ=GGCTGTAGGC"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1924 CTGGCTCGAAGGAAAAGGAATTCTCAGATTCCTCACAGCCATGACAAAGTACAAGATCTG 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 GAT-----GACCTAAAAGCTAACAGTGTCCTTCGTTCTCAGCAACTGTCTAGAACT 2433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2493 AAAGCAGAAAAGAGGTTTGTTTCAGAATGCATGGGAAGAGACCTACGCCAAACCCAGTGT 2552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2613 GAAAG-CAGGAATCTGTAGAGGCGAGGCTGTCTCAACTGCAGAGTGAAAATATGTTGCTT 2671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lysieu---LysGluLysGlnAspLysGluIleLeuGluAlaGluIleGluSerHisHis 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 ProArgleuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSerGln 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 GluProAlaPheHisIleAlaGlyAspAlaCys----LeuGlnArgLysMetAsnVal 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 GlnArgLysSerLysSerLeuLysIleAsnLeuAsnTyrAlaGlyAspAlaLeuArg--- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 -----GluAsnThrLeuValSerGluHisAlaGlnArgAspGlnArgGluThrGlnCys 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --Leulys 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GluLysAsnAlaGluLeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArg 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 AlaSerGlnTyrSerGlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetGlyThrArgAlaLeuGlnCysGluValSerHisThrHisGluAsnGluAsnTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuHisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2044 ATAGAAAACAGAAGAAAATAAAAAGAACTATTTTGAGGACATT------
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                                                                                                                                                                                               3794
143
43
119
25
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Matches:
Conservative:
Mismatches:
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                                    Gaps:
"clone_lib="NIH_MGC_97"
                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-489-079-25 (1-317) x BC036210 (1-3794)
                                                                                                                                                                                           8.3e-45
527.00
56.71%
43.60%
32.29%
                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                        Alignment Scores:
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/db_xref="taxon:1000"
/db_xref="taxon:1000"
/clone="taxon:1000"
/dev_stage="whole brain"
/dev_stage="mbryo 13.5,14.5,16.5,17.5dpc"
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/lab_host="DH10B (TI phage resistant)"
/clone lib="NIH BMAP_PYO"
/note="Torgan: Brain; Vector: pYX- Asc; Site_1: BCOR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand CDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCCAGACAG. This library was created for the University
lows Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Haalth (NIMH), Hemin Chin, Ph.D.,
program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lysteu---LysGluLysGlnAspLysGluIleLeuGluAlaGluIleGluSerHisHis 119
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Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at this://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuLysHisGlnTyrGlnGluLysGluAsnLysTyrPheGluAspileLysIleLeuLys 60
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1113
34
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Matches:
Conservative:
Mismatches:
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::
                                                                                                                                                                           1. .700
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
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                                                                                                                                                                  Location/Qualifiers
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509.50
67.12%
51.60%
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Pred. No.:
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DB:
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                                                                                                                                                                  FEATURES
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UI-M-FYO-Cfi-m-15-0-UI.rl NIH BMAP_FYO Mus musculus CDNA clone IMAGE:6850072 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s-----LeuGlnArgLysMetAsnValAspValSerSerThrIleTyrAsnAsnGluVa 168
                                                                                                                                                                                                                                                                                                                 517
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 700)
                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 TCTTTCTCAACAACTATTTAAAACTGAAAGTAAACTCAATAGCCTAGAAATTGAGTTCCA
                                                                                                                                                                                                                           AlaMetLeuLysLeuGluIleAlaThrLeu-LysHisGlnTyrGlnGluLysGluAsnLy
                                                                                                                                                                                                                                                                                                    sTyrPheGluAspileLysileLeuLysGluLysAsnAlaGluLeuGlnMetThrLeuLy
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                                                                                                                                                                                                         HisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLysLysGluIle
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                          638
116
32
58
5
                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGCCTAAACACAGTGTCAAAAAAAAA
                                                                                                                                                                     (1-638)
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Mus musculus
                                                                                                                                                                       US-09-489-079-25 (1-317) x BU678550
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                                         1.86e-44
513.50
70.14%
54.98%
31.46%
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                                                                                Percent Similarity:
Best Local Similarity:
                           Alignment Scores:
Pred. No.:
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DB:
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DEFINITION

RESULT 9 CN458404

ACCESSION

AUTHORS TITLE JOURNAL COMMENT

FEATURES

ORIGIN

REFERENCE

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BG431116 862 bp mRNA linear EST 14-MAR-2001
602498742F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4612186 5',
                                                                                                                                                                                                        96 ThrMetLeuThrSerLysLeu---LysGluLysGlnAspLysGluIleLeuGluAlaGlu 114
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GTTGAGTCGTTCCGATCTAGGCTGGCTTCTGCTCTGCATGATCACGCTGAAATTCAGACA 120
                                                                                                                                                                                                                                                                                                                                                                                    SerArgLysSerGlnGluProAlaPheHisIleAlaGlyAspAlaCys-----LeuGln 152
                                                                                                                                                                                                                                                                                                                                                                                                                              121 GCAAAAAGAGACCTAGAAATTGCTTTCCAGAGAGCGAGAGATGAGTGGTTTCGTGTAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 ArgLysMetAsnValAspValSerSerThrIleTyrAsnAsnGluValLeuHisGlnPro 172
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11 HAGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                              Conservative:
Mismatches:
Indels:
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/clone="NBAGE:30650305"
/tissue_type="Upper Head"
/dw stage="J.5-10.5 dpc"
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/clone=lib="NIH BMAP HN0"
/note="Organ: Head, Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonnido, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor digested with NotI and then cloned
directionally into pXx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                                                                                                              CM458404 1inear EST 21-APR-2004 UI-M-HNO-coq-m-02-0-UI.rl NIH EMAP_HNO Mus musculus CDNA clone MARE:30650305 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                   GlubroAlaPheHisIleAlaGlyAspAlaCys-----LeuGlnArgLysMetAsnVal 157
                                                                                          464 GAAATTGCTTTCCAGAGAGGGAGAGATGATGGTTTCGTGTGAAAGACAAGATGAATTTC 523
                                                                                                                                         158 AspValSerSerThrIleTyrAsnAsnGluValLeuHisGlnProLeuSerGluAlaGln 177
                                                                                                                                                                   178 ArglysSerLysSerLeuLysIleAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsn 197
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584 AGGAAGTTGAATAGCCTAGAAATTGAGTTTCATCACACGAAAGATGAGGCTTCGAGAAAG 643
      104 TCTAGGCTGGCTTCTGCTCTGCATGATCACGCTGAAATTCAGACAGCAAAAAGAGACCTA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musi
1 (bases 1 to 699)
                                                                                                                                                                                                                                                                                                                   198 ThrLeuValSerGluHisAlaGlnArgAspGlnArgGluThrGlnCysGlnMetLys 216
                                                                                                                                                                                                                                                                                                                                                             644 ACCCTGGCGTTAAAGCATGCGCAGAGACCTGAGCCAGACCCAGTGCCAGATGAAG 700
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Location/Qualifiers
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CN458404.1 GI:46464130
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BP238820 Sugano cDNA library, liver HepG2 Homo sapiens cDNA clone HEP04550, mRNA sequence.
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Suzuki,Y., Yameshita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki,
Department of Virology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                           177 lnArgLysSerLysSerLeuLysIleAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute of Medical Science, University of Tokyo 18titute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yeuzukidaims.u-tokyo.ac.jp.
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/db_xref="taxon:9606"
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470.00
68.00%
53.50%
28.80%
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/mol_type="mRNA"
/mol_type="mRNA"
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/do_type="mRNA"
/do_type="mRNA"
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/clone="longan: Ainley; fortor: pDNR-LIB (Clontech); Site_1:
/note="lorgan: kidney; fortor: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgcccggcccggcc; Site_2: Sfil (ggccattatggcc); Sfil (ggccattatggcc); Sfil (ggccattatggcc); Sfil (ggccattatggcc); Sfil (ggccattatggcc); Sfil (ggc
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                           Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The yet Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI360 row: d column: 11
High quality sequence stop: 730.
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Matches:
Conservative:
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Indels:
        Contact: Robert Strausberg, Ph.D.
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Mismatches:
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BWFZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp781B2319) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
Author: Information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5193 bp mRNA linear HTC 19-AUG-2004
Homo gapiens mRNA; cDNA DKFZp781B2319 (from clone DKFZp781B2319).
CR627244
HTC.
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/tissue type="testis"
/clone_lib="781 (synonym: hlcc4). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
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                          SerLysLeuLys---GluLysGlnAspLysGluIleLeuGluAlaGluIleGluSerHis 118
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1 (bases 1 to 5193)
Kochrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
                                               360 rrrgargreraaceraaagaraacargagarrerrercaacaacrarraaaacr
                                                                                                                                                                                                                                                                                                                   GlnArgiysSerLysSerLeuLysIleAsnLeuAsnTyrAlaGlyAspAlaLeuArgGlu
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Neuherberg, GERMANY
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/note="putative transcript"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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AUTHORS
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197

177

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/mol_type="mRNA" -
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
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                   558 AACGATAGCCCATTATAGTGGACAGCTTACTGCTCTGACAGATGAGAACACAATGCTCCG 499
                                                                                                                                                                                 sProArgieuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSerGl 139
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Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Feng, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L. W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R.
Regenerative Medicine
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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230 Constitution Drive, Menlo Park, CA 94025, USA
121: 650 473 7760
Fax: 650 473 7760
Email: rbrandenbergeron.com
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//organism="Romo sapiens"
//mol_type="mRNA"
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//lab_host="DHJ08 (shage-resistant)"
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//note="Organ: llung' Vector: poTB7; Site_1: XhoI; Site_2: Site_2
AGENCOURT 8795642 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6429928
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(bases 1 to 1014)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTP/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2618 row: o column: 17
High quality sequence start: 24
High quality sequence start: 24
Location/Qualifiers
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43.17%
25.58%
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(MGC)

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1. .886
/organism="HOmo sapiens"
/mol_type="mRNA"
/db &ref="taxon:966"
/clone="IMAGE:6157635"
/tissue_type="melanotic melanoma"
/lab host="DH10B (phage-resistant)"
/clone lib="NHH MGC 72"
/note="Organ: Skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."
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AGENCOURT_7892743 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6157635
5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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461 GAGAGTAAGTCCAGAGTCCATTACACAGGGGGGGCTCTGAAAGAA
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from undifferentiated hES cell lines H1 (p32), H7 and H9 (p26) maintained in feeder-free conditions ^{\rm t}
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Search completed: August 2, 2005, 11:46:07 Job time : 12072.9 secs

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AAB07640 standard; peptide; 44 AA
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1 MQKSVPNKALELKNEQTLRA.....PSESKQKDYEBSSWDSESLC 44
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Aab07640 Amino aci	Aab63909 Human pro	Aab63906 Human pro	Human	Aab63933 Human pro	Human	Aab63918 Human pro	7 Human	Aab63917 Human pro	Human	Aab63901 Human pro	Aab63925 Human pro	Human		Aab07638 Amino aci	Aab50249 Human bre	Aag65987 B726P spl	Human	Abg78917 Human bre	oj37740 Human tum	1193135 Human bre	Ade44425 Human bre	Human	Aag65986 B726P spl	Aau33349 Human bre
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ID	AAB07640	AAB63909	AAB63906	AAB63926	AAB63933	AAB63929	AAB63918	AAB63937	AAB63917	AAB63903	AAB63901	AAB63925	ADB83983	AAB63899	AAB07638	AAB50249	AAG65987	AAU33350	ABG78917	ABJ37740	ADL93135	ADE44425	AAB50248	AAG65986	AAU33349
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ALIGNMENTS

a used BS322-specific polynucleotides, polypeptides and antibodies, used in the detection and diagnosis of breast disease especially breast cancer. The present sequence represents an antigenic peptide derived from human BS322 polypeptide. The peptide is used to raise antibodies. BS322 is a breast tissue marker. The BS322 polymucleotides and polypeptides are use to detect and diagnose breast disease, e.g. breast cancer. The BS322 polymucleotides are useful as a source of probes and primers, and the BS322 polypeptides are useful as antigens Amino acid sequence of an antigenic peptide from BS322 polypeptide. Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon Granados EN, Hodges SC, Klass MR, Kratochvil JD, Russell JC; BS322; breast tissue marker; breast disease; breast cancer, Claim 23; Page 125; 126pp; English. 21-JAN-2000; 2000WO-US001452. 99US-00234716. WPI; 2000-499217/44. (ABBO) ABBOTT LAB. WO200043420-A1. 21-JAN-1999; 27-JUL-2000. Stroupe SD;

Sequence 44 AA;

Gaps ö Query Match 100.0%; Score 225; DB 3; Length 44; Best Local Similarity 100.0%; Pred. No. 9.4e-23; Matches 44; Conservative 0; Mismatches 0; Indels

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RESULT 2 AAB63909

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represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CARP) respectively.

AAB63332 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP artibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate cancer associated antigen protein sequence SEQ ID NO:1288.
                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                Human, breast cancer; gastric cancer; prostate cancer, diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
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iive 0; Mismatches 0;
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10-SEP-1999;
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                                                                                                                                                                                                                                                            Human prostate cancer associated antigen protein sequence SEQ ID NO:1271.
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100.0%; Score 225; DB 4;
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Matches 44; Conservative 0; Mismatches 0;
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                                                                                                                                        AAB63909 standard; protein; 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000; 2000WO-US014749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0136526P.
                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                     WO200073801-A2
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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10-SEP-1999;
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                                                                                                                                                                                AAB63909;
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cancer.

RESULT 3 **AAB63906**

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AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB62232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB631212 to AAB63467, AAB63468 to AAB63701 and AAB63722 to AAB63370.

represent human breast, gastric and prostate CAAP protein sequence respectively. CAAP6 have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate cancer associated antigen protein sequence SEQ ID NO:1291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
                                                                                                                                                                                                                                                                                                      Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                         90 MOKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLC 133
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                             44
                                                                                                                                                                                                                                                                                                                                                                                             1 MOKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLC
                                                                                                                                                                                                                                                                                                      100.0%; Score 225; DB 4;
100.0%; Pred. No. 6.1e-22;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 780; 799pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB63929 standard; protein; 189 AA
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99US-0153454P.
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                                                                                                                                                                                                                                                                                                                                                     44; Conservative
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                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                              Sequence 185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 189 AA;
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10-SEP-1999;
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                                                                                                                                                                                                                   e.g. cancer
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                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                           AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate cancer associated antigen protein sequence SEQ ID NO:1295.
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                                                                                                                                                                    Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 225; DB 4;
; Pred. No. 5.6e-22;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                     Example 1; Page 779; 799pp; English.
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                                     (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 44; Conservative 0;
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                                                                                                                            WPI; 2001-025274/03
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                                                                               Obata Y;
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X8X174778X1X8X8X8X8X8X8X8X8X8X8X8X

AAB6391

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represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. Prostate cancer associated antigen precursors (CAAP) respectively. AAB63123 to AAB63467, AAB63468 to AAB63121 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate cancer associated antigen protein sequence SEQ ID NO:1279.
                                   Human prostate cancer associated antigen protein sequence SEQ ID NO:1299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                           Human, breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
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1 Similarity 100.0%; Pred. No. 7.1e-22;
44; Conservative 0; Mismatchen n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 783-784; 799pp; English
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99US-0153454P.
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26-MAR-2001 (first entry)
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10-SEP-1999;
                                                                                                                                          Homo sapiens
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Matches
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AAB63232 to AAB63467, AAB63468 to AAB63722 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                           Human prostate cancer associated antigen protein sequence SEQ ID NO:1280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gastric and prostate cancer associated diagnosing and treating a condition an abnormal amount of a protein, e.g.
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                       Gaps
                                                                                                                                                                                                                                                                                                                                                                   Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
cancer associated antigen; cytostatic; cancer vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 MQKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLC 121
                                                                                      112 MOKSVPNKALELKNEQTLRADEILPSESKQXDYEESSWDSESLC 155
                     Indels
                                                          1 MOKSVPNKALELKNEQTLRADEILPSESKOKDYEESSWDSESLC 44
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  6.3e-22;
hes 0;
  100.0%; Pred. No. 6.3 iive 0; Mismatches
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                                                                                                                                                                                                       AAB63918 standard; protein; 195 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding breast,
antigen precursors, useful for
characterized by expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                                     (first entry)
                     44; Conservative
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Best Local Similarity
Matches 44; Conserv
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Matches 44; Conserv
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10-SEP-1999;
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                                                                                                                                                                                                                                             AAB63918;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB63937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obata Y;
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Gaps

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44 Indels

RESULT 8

ò 셤 SAXA

Length 207;

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AAF22422 to AAF22656, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precureors (CAAP) respectively. AAB63122 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63467, AAB63467 to AAB63721 and AAB63722 to AAB63467, Gastric and prostate CAAP protein sequence respectively. CAAPE have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                  AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63467, AAB63467 to AAB63721 and AAB63722 to AAB63467, AAB63467 to AAB63721 and AAB63722 to AAB63467 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate cancer associated antigen protein sequence SEQ ID NO:1263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                    Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 MOKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLC 141
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MOKSVPNKALELKNEQTLRADEILPSESKOKDYEESSWDSESLC 44
                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 225; DB 4;
100.0%; Pred. No. 7.8e-22;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 768; 799pp; English.
                Example 1; Page 769; 799pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB63901 standard; protein; 225 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000; 2000WO-US014749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0153454P.
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                                                                                                                                                                                                                                                                                                                                                                                                44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-025274/03.
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                             Sequence 223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200073801-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-DEC-2000.
                                                                                                                                                                                                                                                                 e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. cancer
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                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Obata Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer.
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB63903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                represent nuclectide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB631461 to AAB63122 to AAB63122 to AAB63122 to AAB63122 to AAB63172 to are respectively. Gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate cancer associated antigen protein sequence SEQ ID NO:1265.
                                                                                                                                                                                                                     Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MOKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLC 44
                                                                                                                                                                                                                                                                                                                                      Example 1; Page 775; 799pp; English.
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                                                                                        (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
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                         99US-0136526P.
99US-0153454P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
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                                                                                                                                                                             WPI; 2001-025274/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200073801-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAY-1999;
10-SEP-1999;
                    28-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g. cancer
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                                                                                                                                    Obata Y;
                                                                                                                                                                                                                                                                                               cancer.
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Matches
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The invention related to a combination of polynucleotides. The combination of polynucleotides is useful for preparing a composition for diagnosing or treating cancer or neurodegenerative disorders. The present sequence represents the amino acid sequence of the human breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New combination of polynucleotides, useful for preparing a composition for diagnosing or treating cancer or neurodegenerative disorders.
                                                                             Human breast cancer diagnostic marker protein Incyte 411152.
                                                                                                       cancer; neurodegenerative digorder; human; breast cancer; diagnostic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLC 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MOKSVPNKALELKNEQTLRADEILPSESKOKDYBESSWDSESLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 225; DB 7;
Pred. No. 8.6e-22;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                         CCC.
                                                                                                                                                                                                                                                          GAT"
                                                                                                                                                                                                                                                                                                                                                                                          /note= "Encoded by AGA"
                                                                                                                                                                                                                          'note= "Encoded by GAG"
                                                                                                                                                                                                                                                                                           by AAT"
                                                                                                                                                                                                                                                                                                                         TTT
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                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                         note= "Encoded by
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                                                                                                                                                                                                                                                                                                                         note= "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic marker Incyte 411152.
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100.0%; Pr
:ive 0;
                                                                                                                                                                                                                                                          "Encoded
                                                                                                                                                                                                                                                                                            "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Walker MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2002; 2002US-00133757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-APR-2001; 2001US-0287153P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Conservative
                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                            'note=
                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang C, Mahini B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI: 2003-687833/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZHAN/) ZHANG C.
(MAHI/) MAHINI B.
(WALK/) WALKER M G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                             Misc-difference
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                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                             Misc-difference
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                                                                                                                                                               Homo sapiens.
                                               04-DEC-2003
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                ADB83983;
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                                                                                                                                                                                                                                                                                                            Human prostate cancer associated antigen protein sequence SEQ ID NO:1287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                          Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
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                              Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                    MOKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MOKSVPNKALELKNEQTLRADEILPSESKOKDYEESSWDSESLC 44
                                                              Indels
                                                                                              1 MOKSVPNKALELKNEQTLRADEILPSESKOKDYEESSWDSESLC 44
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                                100.0%; Score 225; DB 4;
100.0%; Pred. No. 7.9e-22;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 225; DB 4;
Pred. No. 8.1e-22;
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                                                                                                                                                                                                              AAB63925 standard; protein; 229
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                                                                                                                                                                                                                                                                             (first entry)
                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-025274/03.
                                               Local Similarity
Les 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
   Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 229 AA;
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                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAY-1999;
10-SEP-1999;
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                                 Query Match
                                                                                                                                                                                                                                               AAB63925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Obata Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer.
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Matches
                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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Gaps .

Indels 44

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Length 241;

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(ABBO ) ABBOTT LAB
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                                                                                                                                                                                                                                                                                                                                                                                     represent nuclectide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63770 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAP8 have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
prostate cancer associated antigen protein sequence SEQ ID NO:1261.
                                                                                                                                                                                                                                                                                   Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                             AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
                         Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 225; DB 4; Length 266; Best Local Similarity 100.0%; Pred. No. 9.8e-22; Matches 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              breast tissue marker; breast disease; breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MQKSVPNKALELKNEQTLRADBILPSESKQKDYBESSWDSESLC 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid seguence of BS322 polypeptide.
                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 767; 799pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB07638 standard; protein; 398
                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                   99US-0136526P.
99US-0153454P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2000; 2000WO-US001452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00234716
                                                                                                                                           26-MAY-2000; 2000WO-US014749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                            WPI; 2001-025274/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200043420-A1
                                                                                        WO200073801-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JAN-1999;
                                                                 Homo sapiens.
                                                                                                                                                                   28-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUL-2000
                                                                                                                07-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
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                                                                                                                                                                                                                                  Obata Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BS322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB07638
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                                                                                                                                                                                                                                                                                                                              The present sequence represents a human BS322 polypeptide. BS322 is a breast tissue marker. The BS322 polynucleotides and polypeptides are used to detect and diagnose breast disease, e.g. breast cancer. The BS322 polynucleotides are useful as a source of probes and primers, and the BS322 polypeptides are useful as antigens
                                                                                                                                                                                          BS322-specific polynucleotides, polypeptides and antibodies, used in the detection and diagnosis of breast disease especially breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
Hodges SC, Klass MR, Kratochvil JD, Russell JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MQKSVPNKALELKNEQTLRADEILPSESKQKDYEESSWDSESLC 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MQKSVPNKALELKNBQTLRADBILPSESKQKDYBESSWDSESLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 225; DB 3;
100.0%; Pred. No. 1.7e-21;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                Claim 23; Page 122-123; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: August 1, 2005, 22:18:04 Job time : 15.6398 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100...
A4; Conservative
                                                                                                                  WPI; 2000-499217/44
     Billing-Medel PA,
Granados EN, Hoc
                                                                                                                                               N-PSDB; AAAS9015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 398 AA;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

August 1, 2005, 22:08:06 ; Search time 2.7109 Seconds (without alignments) 1561.672 Million cell updates/sec Run on:

Title: Perfect score:

US-09-489-079-26 225 1 MOKSVPNKALELKNEQTLRA.....PSESKQKDYEESSWDSESLC 44 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote	chromosomal protei	hypothetical prote	hypothetical prote	related to yeast z	molybdate-binding	molybdate-binding	receiver-like prot	hypothetical prote	DNA topoisomerase	flagellar biosynth	hypothetical prote		probable alpha hel	probable alpha hel	probable alpha hel	endospore developm	hypothetical prote	molybdate-binding	transmembrane prot	O)							hypothetical prote	reverse gyrase - T
SOFTWALES	ΩI	T15945	B55094	T32483	T38616	T39006	G90727	H85578	T04653	G90592	JC6552	F83465	T47279	S51866	A85901	A49940	E91056	C40646	S46775	C64812	AH1140	AC1499	E85508	E90657	T40098	T48800	D64509	C84861	S46838	C72409
	DB	~	~	7	~	~	~	~	~	~	~	~	~	~	~	N	~	~	~	Н	~	~	N	7	7	~	7	~		~
	Query Match Length	629	1203	678	771	938	257	257	552	876	1015	707	173	752	237	237	237	332	554	257	491	491	919	616	274	1240	396	999	713	1104
de	Query Match	27.1	26.9	26.4	26.2	26.2	25.8	25.8	25.6	25.3	25.3	25.1	24.9	24.9	24.7	24.7	24.7	24.7	24.7	24.4	24.4	24.4	24.4	24.4	24.2	24.2	24.0	24.0	24.0	24.0
	Score	61	60.5	59.5	59	59	28	28	57.5	57	57	56.5	26	99	55.5	55.5	55.5	55.5	55.5	55	55	55	55	55		54.5	54	54	54	54
	Result No.		8	m	4	ហ	9	7	8	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

1;

Gaps

1;

Ouery Match 26.9%; Score 60.5; DB 2; Length 1203; Best Local Similarity 40.5%; Pred. No. 46; Matches 15; Conservative 8; Mismatches 13; Indels 1;

natural killer cel hypothetical prote	coat protein - pop hypothetical prote hypothetical prote	hypothetical prote conserved hypothet	hypothetical prote serine/threonine p	alpha-A-crystallin hypothetical prote	protein T05G5.1 [i	heat shock protein	heat shock protein	capsid protein - h
A47328 G96585	JQ1645 T45869 T21336	T02570 B97992	T32251 T17365	149477 S41001	F88563	E83234 T39202	851795	S45048
4 2	- 0 C	0 0	0 0	0 0	0	v 0	~	7
1403	322 511 817	189	375	2688 346	412	4 4 4 7 0 4	704	771
24.0	2 2 2 2 3 3 3 3 8 8 8	23.6	23.6	23.6	23.3	23.3	23.3	23.3
54		23	23	53	52.5	52.5	52.5	52.5
30	W W W	36	37	0.4 0.0	41	4 4 2 6	44	45

ALIGNMENTS

	RESULT 1
_	hypothetical protein FOIFL.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20.5ep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
	S, Miller, N. submitted to the EMBL Data Library, July 1995 A, Description: The sequence of C. elegans cosmid FOIF1. A, Reference number: Z18435
	A, Accession: T15945 A, Status: preliminary; translated from GB/EMBL/DDBJ A, Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: DNA A, Residues: 1-629 < MIL> A, Cross-references: UNIPROT: Q19086; EMBL: U13070; NID: G529697; PID: G529702; PIDN: AAC4663 A, Experimental source: strain Bristol N2
· * * · · · · · · · · · · · · · · · · ·	C;Genetics: A;Gene: CES: A;Introns: 120/2; 286/3; 384/1; 478/2 C;Superfamily: Synechocystis hypothetical protein slr0825
	Query Match 27.1%; Score 61; DB 2; Length 629; Best Local Similarity 32.1%; Pred. No. 19; Matches 18; Conservative 5; Mismatches 15; Indels 18; Gaps 2;
	QY 1 MQKSVPNKALELKNEQTLEADEILPSESKQKDYEESSWDSESL 43
	RESULT 2 B55094 chromosomal protein XCAP-E - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Species: Anar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004 C;Accession: B55094
	Rifirano, T.; Mitchison, T.J. Cell 79, 449-458, 1994 A; Title: A heterodimeric coiled-coil protein required for mitotic chromosome condensati A; Reference number: A55094; MUID:95042742; PMID:7954811 A; Accession: R55084
	Attactus: preliminary Attactus: preliminary Attactus: preliminary Attactus: preliminary Attactus: preliminary Attactus: ncondension of the state of

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A;Residues: 1-938 <PUR>
A;Residues: 1-938 <PUR>
A;Cross-references: UNIPROT:014100; EMBL:AL034583; PIDN:CAA22593.1; GSPDB:GN00066; SPDB: A;Cross-references: UNIPROT:014100; EMBL:AL0317
C;Genetics: A;Gene: SPAC31F12.01; SPDB:SPAC637.14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molybdate-binding periplasmic permease protein [imported] - Escherichia coli (strain Ols C;Species: Bscherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: 690727
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res 8, 11-22, 2001
A;Ritle: Complete genome sequence of enterohemorrhagic Escherichia coli Ol57:H7 and genomaly A;Reference number: A99629; MUID:21156231; PMID:11228796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27 «HAX»
A;Cross-references: UNIPROT:Q8X931; GB:BA000007; PIDN:BAB34214.1; PID:g13360250; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: H85578

C;Accession: H85578

T; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhewi N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J. D.; Rose, D.J.; Mayhewi Iller, L.; Grocheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-raferences: UNIPROT:Q8X931; GB:AE005174; NID:g12513695; PIDN:AAG55092.1; GSPDB:G.A,Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85578
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16;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 938;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 OKSVPNKA--LELKNEQTL----RADEILPSESKOKDYBES 36
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C;Superfamily: molybdate-binding periplasmic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: molybdate-binding periplasmic protein
                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                             2;
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Best Local Similarity 30.4%; Pred. No. 16;
Matches 14; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 25.8%; Score 58; DB 1 Similarity 30.4%; Pred. No. 16; 14; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.2%; Score 59; DB Best Local Similarity 39.0%; Pred. No. 52; Matches 16; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-257 <STO>
A; Accession: T39006
                                                                                                                                                                                                                                                                                                                                A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: ECs0791
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                                                                                                                                                                                                                                                                    hypochetical protein F52H2.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: 29-oct-1999 #sequence_revision 29-oct-1999 #text_change 09-Jul-2004
C; Accession: T33483
R; Chissoe, S: Hawkins, J.
Submitted to the EMBL Data Library, September 1997
A; Description: The sequence of C. elegans cosmid F52H2.
A; Reference number: 221175
A; Accession: T3483
A; Accession: T3483
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-678 <CHI>A; Residues: 1-678 <CHI>A; Residues: 1-678 <CHI>A; Residues: 1-678 <CHI
A; Residues: 1-678 <CHI
A; Residues: 1-678 <CHI
A; Residues: 1-678 <CHI
A; Roperimental source: strain Bristol N2; clone F52H2
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Map position: X
A; Introns: 53/3; 96/3; 132/3; 169/3; 249/2; 373/3; 638/1
C; Superfamily: Caenorhabditis elegans hypothetical protein F52H2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypochetical protein SPAC31F12.01 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004
C;Accession: T38616
C;Genetics: Committee Committee Committee Committee Committee Committee Committee Committee Committee C;Cometics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Cenetics: C;Cene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.4%; Score 59.5; DB 2; Length 678; Best Local Similarity 42.9%; Pred. No. 31; Matches 15; Conservative 7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.2%; Score 59; DB 2; Length 771; 39.0%; Pred. No. 42; ive 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 EDSVPSKSSVLEDKHENSVEIDKKADDSLPSNNKTEGYTPS 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QKSVPNKA--LELKNEQTL----RADEILPSESKQKDYEES 36
                                                           182 QKTIEKKEAKLKEIQTILEEEITPTIHKLKE-ERSSY 217
    QKSVPNKALELKNEQTLRADEILPSESKQKDYEESSW 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      619 KRNKKNKAKELQKEQPLR-HQFRPTKSKFNDYLSS 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: SPDB:SPAC31F12.01
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    8
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C;Accession: JC6552
R;Czerwinski, R.M.; Lipniacki, A.; Staron, K.
R;Czerwinski, R.M.; Lipniacki, A.; Staron, K.
A;Title: CDNA cloning of Physarum polycephalum DNA topoisomerase I and expression analy A;Reference number: JC652; MUID:98245940; PMID:9583949
A;Accession: JC6552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A,Reference number: A82950, MUID:20437337, PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A,Residues: 1-707 <STO>
A,Cross-references: UNIPROT:Q913P9; GB:AE004574; GB:AE004091; NID:g9947391; PIDN:AAG048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F26B15.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47279
R;Nyakatura, G:; Fartmann, B:; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-1015 <CZE>
A;Cross-references: UNIPROT:Q94705; GB:AF023910; GB:U63217; NID:g2642492; PIDN:AAC14193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flagellar biosynthesis protein FlhA PA1452 [imported] - Pseudomonas aeruginosa (strain C; Species: Pseudomonas aeruginosa (c; Species: Pseudomonas aeruginosa (c; Species: Pseudomonas aeruginosa (c; Species: Pseudomonas aeruginosa (c; Spaces) (c; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Badman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim Nature 406, 959-964, 2000
                                                                                                 DNA topoisomerase (EC 5.99.1.2) - slime mold (Physarum polycephalum)
N;Alternate names: emega-protein; micking-closing enzyme; type I DNA topoisomerase
C;Species: Physarum polycephalum
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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submitted to the Protein Sequence Database, April 2000
A,Reference number: Z24458
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NKAKQVAEQEVQRQQELLPAQRAQ-EVKELGWD 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Superfamily: eukaryotic type I DNA topoisomerase C.Keywords: isomerase P:974/Active site: Tyr #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 NKALELKNEQTLRADEILPSESKOKDYBESSWD 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 25.3%; Score 57; DB 1 Similarity 34.2%; Pred. No. 99; 13; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Mismatches
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25.1%; Score 56.5;
Best Local Similarity 33.3%; Pred. No. 75
Matches 11; Conservative 9; Mismatche
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A,Gene: flhA, PA1452
C,Superfamily: regulatory protein lcrD
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Best Local Similarity
Matches 13; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
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                                                                                                                                                                                                                                                         reciver-like protein 4 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04653; T25035
R;Beron, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15263
A;Rocleule type: DNA
A;Residues: 1-52 cBEV>
A;Residues: 1-52 cBEV>
A;Cross-references: UNIPROT:049397; EMBL:ALO21636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A. Experimental source: cultivar Columbia; Decorporation F10N7
R. Buchholz, G.; Keitel, C.; Kircher, S.; Kudla, J.; Lohrmann, J.; Sweere, U.; Schaefer, submitted to the EMBL Data Library, May 1998
A. Possoription: Nuclear-localized receiver-like proteins are differentially expressed in A. Reference number: Z25912
A. A. Scession: T52035
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Residues: 1-552 < CONCS A. Residues: L-552 < CONCS A. COSS - references: EMBL. AJ005195; PIDN: CAA06432.1
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R; Chambaud, I:, Hellig, R:, Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; R; Chambaud, I:, Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A; Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A; Reference number: A99512; MUD:21267165; PMID:11353084
A; Accession: G90592
A; Residual G90592
A; Residual G90592
A; Residual Syfe ckUR>
A; Residual surverses: UNIPROT:098PS2; GB:AL445566; PID:g14090062; PIDN:CAC13820.1; GSPDB:CAC13820.1; G
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C,Species: Mycoplasma pulmonis
C,Date: 24-May_2001 #sequence_revision 24-May_2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: response regulator, ARR1 type; response regulator homology
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                                              Length 876;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
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84;
1 MOKSVPNKALELKNEQTLRADEIL---PSESKOKDY
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Pred. No. 84;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 25.6%; Score 57.5; DE Local Similarity 30.4%; Pred. No. 43; Nes 17; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 4
A;Introns: 43/1; 94/1; 207/1; 232/3; 517/3
A;Note: F10N7.270
C;Superfamily: response reculator. ARP1 tur
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Best Local Similarity 36.8%;
Matches 14; Conservative 7
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A;Cross-references: GB:AE005174; NID:g12516965; PIDN:AAG57669.1; GSPDB:GN00145; UWGP:Z38 A;Experimental source: strain 0157:H7, substrain EDL933 A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-237 <-LIU>
A;Residues: 1-237 <-LIU>
A;Residues: 1-237 <-LIU>
A;Cross-references: UNINROT:P37328; GB:S67014; NID:g455660; PIDN:AAB28777.1; PID:g455661
A;Note: sequence extracted from NCBI backbone (NCBIN:139878, NCBIP:139880)
B;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Residues: 1-237 <BLAT>
A,Cross-references: GB:AE000341; GB:U00096; NID:g1788999; PIDN:AAC75608.1; PID:g1788906;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disobable alpha helix protein [imported] - Escherichia coli (strain K-12) C; Species: Escherichia coli (c)ader: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C; Accession: A49940; B65033 R; Liu, J.; Magasanik, B. J. Bacceriol. 175, 7441-7449, 1993 A; File: The glnB region of the Escherichia coli chromosome. A; File: The glnB region of the Escherichia coli chromosome.
                                                                                                                                                                                                                                                               DB 2; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 277, 1453-1462, 1997
Affittle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B65033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 ALELKNEQT----LR----ADEILPSESKQ--KDYEESSWDS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 ALELKNEQT----LR----ADEILPSESKQ--KDYEESSWDS 40
                                                                                                                                                                                                                                                               24.7%; Score 55.5; D
32.6%; Pred. No. 29;
cive 12; Mismatches
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                                                                                                                                                                                                                                                                                                     Best Local Similarity 32.6
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Conservative
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S51866
HPR1 protein - yeast (Saccharomyces crevisiae)
N;Alternate names: protein YD9302.14; protein YDR138w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995
R*01iver, N: Natris, Data Library, February 1995
R;Oliver, K: Harris, Data Library, February 1995
A;Reference number: S51865
A;Molecule type: DNA
A;Resference number: S51853
A;Accession: S51866
A;Molecule type: DNA
A;Resferences: UNIPROT: P17629; EMBL: Z48179; NID: 9665657; PIDN: CAA88220.1; PID: 96656
A;Molecule type: DNA
A;Coss-references: UNIPROT: P17629; EMBL: Z48179; NID: 9665657; PIDN: CAA88220.1; PID: 96656
A;Molecule type: DNA
A;Accession: A34781
A;Molecule type: DNA
A;Resferences: EMBL: M30484; NID: 9171701; PIDN: AA34685.1; PID: 9171702
A;Cross-references: EMBL: M30484; NID: 9171701; PIDN: AA34685.1; PID: 9171702
A;Cross-references: EMBL: M30484; NID: 9171701; PIDN: AA34685.1; PID: 9171702
A;Cross-references: SGD: HRPA
A;Accession: A;Acserences: EMBL: M30484; NID: 9171701; PIDN: AA34685.1; PID: 9171702
A;Cross-references: EMBL: M30484; NID: 9171701; PIDN: AA34685.1; PID: 9171702
A;Cross-references: EMBL: M30484; NID: 9171701; PIDN: AA34685.1; PID: 9171702
A;Cross-references: EMBL: M30484; NID: 9171701; PIDN: AA34685.1; PID: 9171702
A;Cross-references: EMBL: M30484; NID: 9171701; PIDN: AA34685.1; PID: 9171702
A;Cross-references: EMBL: M30484; NID: 9171701; PIDN: AA34685.1; PID: 9171702
A;Genetics: A;Map position: AR
C;Superfamily: Saccharomyces cerevisiae HPRI protein
C;Keywords: transmembrane protein
F;253-269/Domain: transmembrane #status predicted <TMM>F;253-269/Domain: transmembrane
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A85901
A85901
A85901
Cycbable alpha helix protein yfhG [imported] - Escherichia coli (strain O157:H7, substra
Cyspecies: Escherichia coli
Cybate: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 14-Sep-2001
Cybate: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 14-Sep-2001
Cybate: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 14-Sep-2001
RyPerna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
Ayrithe: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
Ayrecession: A85901
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                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 173;
A;Accession: T47279
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <NYA>
A;Residues: 1-173 <NYA>
A;Experimental source: Cultivar Columbia; BAC clone F26B15
C;Genetics:
A;MAP position: 3
A;Introns: 64/2
A;Note: F26B15.10
C;Superfamily: Arabidopsis thaliana hymorhatical nettice:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 24.9%;
Best Local Similarity 31.8%;
Matches 14; Conservative 8
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homo sapien homo sapien homo sapien

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plasmodium

lotus japon fusobacteri homo sapien

white spot anopheles

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MEDLINE=21174979; PubMed=11280766;

MEDLINE=21174979; PubMed=11280766;

MEDLINE=21174979; PubMed=11280766;

Moder D., Stockert E., Guere A.O., Scanlan M.J., Karbach J.,

Jaeger E., Knuth A., Old L.J., Chen Y.T.;

"Identification of a Tissue-specific Putative Transcription Factor in

Breast Tissue by Serological Screening of a Breast Cancer Library.";

Cancer Res. 61:2055-2061 [2001].

BREL; AP269087; AAX27325.1;

GO; GO:0005514; C:nucleus; NAS.

GO; GO:0005515; F:procein binding; NAS.

GO; GO:0005516; F:procein binding; NAS.

GO; GO:0005510; F:transcription factor activity; NAS.

GO; GO:0005510; F:transcription factor activity; NAS.

InterPro; IPR00110; ANK.

InterPro; IPR001969; Pept_Asp_AS.

RINTS; PR01415; ANK REPEAT; 4.

SNART; SM00248; ANK, REPEAT; 4.

PROSITE; PS50088; ANK REPEAT; 4.

PROSITE; PS50089; ANK_REPEAT; 4.

PROSITE; PS50089; ANK_REPEAT; 4.

PROSITE; PS50089; ANK_REPEAT; 4.

PANSOTIE; PS50089; ANK_REPEAT; 4.

PANSOTIE; PS50089; ANK_REPEAT; 4.

PANSOTIE; PS50089; ANK_REPEAT; 4.

PANSOTIE; PS50097; ANK_REPEAT; 4.

PANSOTIE; PS50089; ANK_REPEAT; 4.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                               Q7kvw1
Q96hm2
Q9btx2
Q9nvm5
Q9nvm9
Q7xe90
Q7rhe8
Q9bbn6
Q7p516
                                                                                                                                                                                                                                                                                                   07pxd8
091199
Q7xpn5
Q9w4c4
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Breast cancer antigen NY-BR-1.1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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100.0%; Pred. No. 8.5e-17;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1341 AA
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07XPN5
099W4C4
07WW1
07WW1
096HN2
09BTX2
09NWM5
07NE90
07XE90
07XE90
07XE90
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01-MAR-2004 (TrEMBLrel. 26, Lat
Breast cancer antigen NY-BR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 17,
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     548
585
607
706
706
1066
11654
11793
1134
209
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     O9BXX3;
01-JUN-2001 (
01-JUN-2001 (
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SEQUENCE
     Query Match
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Q9BXX2
ID, Q9BX
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Q9BXX3
       SOW WHEN THE PRICE OF THE PRICE
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Q8i3j9 plasmodium
Q8x31 escherichia
Q83sa5 shigella f1
Q9nw22 homo sapien
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caenorhabdi
escherichia
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                                                                                                                                                                                  August 1, 2005, 22:05:16 ; Search time 12.3033 Seconds
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                                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Q9CAF6
SMC2_XENLA
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Maximum Match 100%
Listing first 45 summaries
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Q6LXV6
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Q9H0H6
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2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Nature 419:498-511(2002).
EMBL; AB014839; AAN35816.1; -.
              0902W8;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
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Les 13; Conservative
 PRELIMINARY;
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ORFNames=PF11_0232;
                                                                              Dnaj-like protein.
                                                                                                                                                                       SEQUENCE FROM N.A
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                                                                                                                                       NCBI_TaxID=10116;
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01-MAR-2003
01-MAR-2003
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                                                                         MEDLINE-21174979; PubMed=11280766;
Jaeger D., Stockert E., Guere A.O., Scanlan M.J., Karbach J.,
Jaeger E., Knuth A., Old L.J., Chen Y.T.;
Indentification of a Tissue-specific Putative Transcription Factor in
Breast Tissue by Serological Screening of a Breast Cancer Library.";
Cancer Res. 61:2055-2061(2001).
EMBL; APZ69089; AAKZ7326.1; -.
InterPro; IPR002110; ANK.
InterPro; IPR002110; ANK.
SMART; SM00248; ANK, 3.
PROSITE; PS50088; ANK REPEAT; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 8.5e-12;
4; Mismatches 5; Indels
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PROSITE; PS50297; ANK REP REGION; 1.
ANK repeat; Hypothetical protein.
SEQUENCE 823 AA; 93968 MW; 9D2DDD5F52C379B2 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp434A171.
Name=DKFZp434A171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    823 AA
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Best Local Similarity 79.5%;
Matches 35; Conservative
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TISSUE=Testis;
The German cDNA Consortium;
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PRINTS; PR01415; ANKYRIN.
SMART; SMO0248; ANK; 6.
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                                                              SEQUENCE FROM N.A.
                              NCBI_TaxID=9606;
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01-MAR-2001
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Wang L., Miao S., Yang J., Zhang X., Zhao M., Li M.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF154849; AAD53061.1; -.
HSSP; P25685; IHDJ.
InterPro; IPR010523; DnaJ. N.
Ffam; PF002245; DnaJ; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS00636; DNAJ_2; 1.
SEQUENCE 223 AA; 25756 MW; EBB4ADFC3CC92D3F CRC64;
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Pred. No. 2e+02;
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SEQUENCE 851 AA; 101937 MW; 466174BC463FD823 CRC64;
               Last sequence update)
Last annotation update)
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Last annotation update)
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41.3%; Pred. No. 40, .... 5; Mismatches
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STRANIE-STRAL/6.1; IISSUE-Testis;
The FANTOM CONSORtium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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STRAIR=C57BL/6J; TISSUB=Testis;
MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Anno H.,
Arakawa T., Bano H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itch M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Koya M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Ttoh M., Aizawa K., Nagaoka S., Saaaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Saaaki N., Carninci P., Sunco H., Akiyama J., Nishihi K., Hazama M., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa W., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikki ihtegrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MUS musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4930483N21 product:similar to DNA-LIKE PROTEIN.
Name=4930503B20Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                 226 AA.
                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN FANTOM Consortium;
                                                 PRELIMINARY;
                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                 Q9D5A2
RESULT 6
                            09D5A2
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MEDLINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F.; Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

By Lischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Reha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Kzywinski M.I., Sakalska U., Smailus D.E., Schnerch A., Schein J.B.,

Jones S.J., Marra M.A.;

and mouse cubik sequences "."

"" And mouse cubik sequences "" and "" 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 61; DB 2; Length 226;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Indels
   to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                    PFam; PF00226; DnaJ; 1. — SMART; SM00271; DnaJ; 1. — PROSITE; PSS0076; DNAJ 2; 1. SEQUENCE 226 AA; 25977 MW; A22055BBC8694599 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18J 2; 1.
26907 MW; C2E8D7EB71AFC9C CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 KALELKNEQTLRADEILPSESKQKDYEESSWD 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 EAAEEKFKQVAEAYHILSDAKKRKDYDRSRWN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      27.1%; Score bi, --40.6%; Pred. No. 61; +ive 5; Mismatches
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GO; GO:0006739; C:mitochondrion;
InterPro; IPR001623; DnaJ.N.
Pfam; PP00226; DnaJ; 1.
                                                                                                            MGD; MGT:1922264; 4930503B20Rik.
GO; GO:0005739; C:mitochondrion;
InterPro; IPR001623; DnaJ_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24,
25,
Submitted (JUL-2000) to the EMBL; AK015617; BAB29906.1; HSSP; P25685; 1HDJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (MAR-2003) to the
EMBL; BC048658; AAH48658.1;
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 40.6'
Matches 13, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00271; DnaJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4930503B20Rik protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=4930503B20Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P25685; 1HDJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissum=Testis;
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DB 2;

Score 61;

27.1%;

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InterPro; IPR005743; DNA_gyrA.
InterPro; IPR006691; DNA_gyraseA_C.
InterPro; IPR002205; DNA_topoisoIV.
Pfam; PF00329; DNA_gyraseA_C; 5.
Pfam; PF00521; DNA_topoisoIV; 1.
ProDom; PD000742; DNA_topoisoIV; 1.
                                                    NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 61; DB 2; Length 629;
Pred. No. 1.9e+02;
5; Mismatches 15; Indels
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The sequence of C. elegans cosmid F01F1.";
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WormBase Consortium;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; U13070; AAC46639.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Tolb_C.
69602 MW; CIEBB9D31799E5F7 CRC64;
                                                                                                                                                                                                                                                            01-NOV-1996 (TTEMBLrel. 01, Last sequence update) 01-OCT-2003 (TTEMBLrel. 25, Last annotation update) 10-OCT-2003 (TTEMBLrel. 25, Last annotation update) 10-OCT-2003 (TTEMBLrel. 25, Last annotation 4. Name-edge-4; ORPNames-F0lFl.5; Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative DNA gyrase A subunit.
Name=TYM13.23;
Arabidopsis thaliana (Mouse-ear cress).
                     14;
                                                          8 KALELKNEQTLRADEILPSESKQKDYEESSWD 39
                                                                                    899 AA
                                                                                                                                                                                                     629 AA
40.6%; Pred. No. 63; ive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; T15945; T15945.
WormBase; WBGene00001057; dpf-4.
WormCep; F01F1.5, CE01231.
GO GO:00105787; F:hydrolase activity; IEA.
InterPro; IPR001379; Ser estra.
InterPro; IPR011042; TolB_C.
                                                                                                                                                                                                                                           1-NOV-1996 (TrEMBLrel. 01, Created)
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                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 32.1
Matches 18; Conservative
                     13; Conservative
                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miller N.; "The sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                629 AA;
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=Bristol N2; Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                        019086;
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09SG75
ID 09SG
DT 01-M
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OS Name
                       Matches
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| March | Marc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003518; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
GO; GO:0006265; P:DNA topological change; IEA.
GO; GO:0006268; P:DNA topoisogical change; IEA.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu
Maiti R., Konning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ï
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas
Lin X., Kaul S., Town C.D., Utterback T.R., Barnstead
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AC011708; AAF19580.1;
HSSP; P09097; 1AB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ACOLISO; AAGS1377.1; -.
HSSP; P09097; 1AB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.9%; Score 60.5; DB 2;
43.8%; Pred. No. 3.2e+02;
tive 8; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 ALELKNEOTLRADEILPSESKOKDYEESSWDS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  917 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence
01-OCT-2003 (TrEMBLrel. 25, Last annotation putative DNA gyrase subunit A; 1114-7603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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SEQUENCE FROM N.A.
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QBKRC9
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                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    888
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION IN A CONDENSIN COMPLEX WITH XCAP-C; XCAP-H; XCAP-D2 AND
                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
05-JJL-2004 (Rel. 44, Last annotation update)
structural maintenance of chromosome 2 (Chromosome-associated protein
B) (Chromosome assembly protein XCAP-E).
Name=SMC2; Synonyms=XCAP-E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION OF THE CONDENSIN COMPLEX.
MEDILINE-99354989; PubMed=10428035; DOI=10.1016/S0092-8674(00)81018-1;
Kimura K., Rybenkov V.V., Crisona N.J., Hirano T., Cozzarelli N.R.;
"13S condensin actively reconfigures DNA by introducing global
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION OF THE CONDENSIN COMPLEX.
MEDLINE=98447791; PubMed=9774278; DOI=10.1126/science.282.5388.487;
Kimura K., Hirano M., Kobayashi R., Hirano T.;
Phosphorylation and activation of 138 condensin by Cdc2 in vitro.";
science 282:487-490(1998).
                                                                                                                                                                                                                                                                                                                  Hirano T., Mitchison T.J.; "A heterodimeric colled-coil protein required for mitotic chromosome condensation in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97304380; PubMed=9160743; DOI=10.1016/S0092-8674(00)80233-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i - FUNCTION: Central component of the condensin complex, a complex
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND INTERACTION WITH XCAP-C.
MEDLINE=95042742; PubMed=7954811; DOI=10.1016/0092-8674(94)90254-2;
                                                                                                                                                                                                                                                                                                                                                                                                Hirano T., Kobayashi R., Hirano M.; "Condensins, chromosome condensation protein complexes containing XCAP-C, XCAP-E and a Xenopus homolog of the Drosophila Barren
                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                           ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             positive writhe: implications for chromosome condensation.";
Cell 98:239-248(1999).
                                       Length 917;
                                                           Indels
SMART; SM00434; TOP4c; 1.
TIGRPAMs; TIGR01063; gyra; 1.
SEQUENCE 917 Aa; 101412 Mw; 7568C4004D524976 CRC64;
                                       26.9%; Score 60.5; DB 2;
43.8%; Pred. No. 3.3e+02;
iive 8; Mismatches 9;
                                                                                        9 ALELKNEQTLRADEILPSESKOKDYEESSWDS 40
                                                                                                                                                    PRT; 1203 AA.
                                                                                                                                                                        (Rel. 34, Created)
                                                 Local Similarity 43.8
les 14; Conservative
                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 89:511-521(1997).
                                                                                                                                                                                                                                                                                                                                                Cell 79:449-458(1994)
                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
                                                                                                                                                                       01-OCT-1996
                                                                                                                                                    XENLA
                                         Query Match
                                                                                                                                                             P50533;
                                                  Best Loc
Matches
                                                                                                                                           XENLA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                similarity).

DOMAIN: The hinge domain, which separates the large intramolecular coiled coil regions, allows the heterodimerization with XCAP-C, forming a V-shaped heterodimer (By similarity).

SIMILARITY: Belongs to the SMC family. SMC2 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromatin. At the onset of prophase, the regulatory subunits of the complex are phosphorylated by CDC2, leading to condensin's association with chromosome arms and to chromosome condensation.
                                                                         Dissociation from chromosomes is observed in late telophase (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fram; PF02463; SMC_N; 1.
ATP-binding; Cell cycle; Coiled coil; DNA condensation; Mitosis; Nuclear protein.
NP BIND 39 ATP (DATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>,</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 669 Flexible hinge.
670 1032 Colled coll (Potential).
105 1121 Ala/Asp-rich (Da-box)
1203 AA; 136341 MW; 04323DD0027DP309 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Indels
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GO:0006250; P:DNA replication; IEA.
GO:0006457; P:protein folding; IEA.
GO:0006986; P:response to unfolded protein; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 QXTIEKKBAKLKEIQTILEEEITPTIHKLKE-ERSSY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QKSVPNKALELKNEQTLRADEILPSESKOKDYEESSW 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 60.5; DB 1;
Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003405; SMC_C.
InterPro; IPR010935; SMC_hinge.
InterPro; IPR003395; SMC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U13674; AAA64680.1; -. PIR; B55094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 40.5
les 15; Conservative
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513
669
1032
1121
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                    Waterston R.;
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DOI=10.1128/AEM.69.9.5070-5078.2003;
Campbell B.J., Stein J.L., Cary S.C.;
Evidence of chemolithoautotrophy in the bacterial community associated with Alvinella pompejana, a hydrothermal vent polychaete.";
Appl. Environ. Microbiol. 69:5070-5078(2003).
                                                                                                                                                                                                                                                                                                                                                           Gaps
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01-OCT-2003 (TrEMBIrel. 25, Last annotation update)
Name-F52H2.1; ORFNames=F52H2.1.
Name-F52H2.1; ORFNames=F52H2.1;
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                            PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
SEQUENCE 391 AA; 40914 MW; 195A823B861BBFCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alvinella pompejana epibiont 7G3.
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
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                                                                                                                                                                                                                                                                                                                  DB 2; Length 391;
                                                                                                                                                                                                                                                                                                                                                           16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 MKLKVPNKVLEVENIDT-KSNTILPLEGYYKLKEGNFLYSENS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MOKSVPNKALELKNEQTLRADEILPSES--KOKD----YEESS 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24167 MW; 8617AEFB26A1F13F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            7 NKALELKNEQTLRADEILPSESKQKDYEESSWDSESL 43
                                                                                                                                                                                                                                                                                                                  26.7%; Score 60; DB 2; 3 40.5%; Pred. No. 1.4e+02; iive 6; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    678 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 AA
InterPro; IPR002939; DnaJ_C.
InterPro; IPR001305; DnaJ_CXXCXGXG.
InterPro; IPR001305; DnaJ_N.
InterPro; IPR001305; HSP40_DnaJ_pep.
InterPro; IPR0013095; HSP_DnaJ_pep.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00586; DnaJ; 1.
Pfam; PF00685; DnaJ_CXXCXGXG; 1.
Pfam; PF00685; DnaJ_CXXCXGXG; 1.
PRINTS; PR00625; DNaJPROTEIN.
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 40.5<sup>3</sup>
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campylobacteraceae.
NCBI_TaxID=244800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=NT03AP0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipoprotein.
SEQUENCE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q6W3L3;
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Q6W3L3
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GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA. GO; GO:0015412; F:molybdate-transporting ATPase activity; IEA. GO; GO:0005215; F:transporter activity; IEA. GO; GO:0005216; P:transporter activity; IEA. GO; GO:0015689; P:molybdate ion transport; IEA.
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MEDLINE=2238024; PubMed=12471157; DOI=10.1073/pnas.255259799;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Welch R.A., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnaneberg M.S., Blattner F.R.;
Catensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
HSSP; P37229; IWOD.
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Enterobacteriaceae, Escherichia.
                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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STRAIN=Bristol N2;
Chissos S., Hawkins J.;
"The sequence of C. elegans cosmid F52H2.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
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EMBL, AF026214, AAB71311.1; -
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01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
MO1ybdate-binding periplasmic protein.
Name=modA; OrderedLocusNames=c0840;
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42.9%; Pred. No. 3e+02;
:ive 7; Mismatches 12;
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Wormbase; WBGene00018714; F52H2.1.
Wormber; F52H2.1a; CB10864.
Hypothetical protein.
SEQUENCE 678 AA; 78262 MW; 49A
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nes 15; Conservative
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Submitted (JUN-2003)
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STRAIN=Bristol N2;
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WormBase Consortium;
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DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IRR011589; MuBP prokaryotic.

DR InterPro; IRR005990; MolP ABC transpt.

DR InterPro; IRR0010916; NolP Bac_I.

DR InterPro; IRR010916; NolP Box_N.

DR Pfam; PP01547; SBP Dac_I; I.

DR PRODITE; PR000430; TONB_DEPENDENT_REC_I; UNKNOWN_I.

DR PROSITE; PS00430; TONB_DEPENDENT_REC_I; UNKNOWN_I.

KW Complete protecome.

SQ SEQUENCE 257 AA; 27414 MW; CECFE98ED902AE87 CRC64;

Query Match

Query Match

Best Local Similarity 30.4%; Pred. No. 1.2e+02;

Matches 14; Conservative 12; Mismatches 14; Indels 6; Gaps 2;
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Search completed: August 1, 2005, 22:22:18 Job time : 16.3033 secs

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BD271305

Reagents and methods useful for detecting diseases of the breast.

BD271305

BD271305

JP 2002540761-A/2.

Homo sapiens

Homo sapiens
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JP 2002540761-A/2
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21-JAN-2000 JP 2000594836
21-JAN-1999 US 09/224716
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1. (bases 1 to 278)
Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Russell, J.C. and Stroupe, S.D.
Reagents and methods useful for detecting diseases of the breast Patent: JP 2002540761-A 2 03-DEC-2002;
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                                    C12P21/02,C12Q1/68,G01N33/53,G01N33/53,G01N33/566,G01N33/574,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of breast cancer
Patent: WO 0151628-A 4060 19-UUL-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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                                               G01N37/00,
C12N15/00,C12N5/00
Reagents and methods useful for detecting diseases of
                                                                            rce Location/Qualifiers 1. 278 /organism='Homo sapiens (human)'.
Location/Qualifiers 1. 278
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Sequence 4060 from Patent W00151628.
CQ419026.
CQ419026.1 GI:41371255
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/db_xref="taxon:9606"
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Best Local Similarity:
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                                                                          21 AspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSer 40
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of breast cancer
Patent: WO 0151628-A 8681 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Novel genes, compositions, kits, and methods for identification,
                  MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla
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Sequence 8681 from Patent WO0151628.
CQ423647.1 GI:41375876
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Homo sapiens
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Homo sapiens
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Best Local Similarity:
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PAT 28-JAN-2004

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Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of breast cancer
Patent: WO 015128-A 11497 19-UL-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Sequence 12497 from Patent WO0151628.
CQ427463
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Homo sapiens
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408 GAGAGTCTCTGT 397
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Best Local Similarity:
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of breast cancer
Patent: WO 0151628 A 12778 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
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assessment, prevention, and therapy of breast cancer Patent: WO 0151628-A 17529 19-JUL-2001, Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Sequence 12778 from Patent W00151628.
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/mol_type="unassigned DNA"
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Homo sapiens
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165 GAGAGTCTCTGT 176
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Best Local Similarity:
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PAT 22-JUN-2001

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
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Indels:
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LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
Location/Qualifiers
Location/Aulaine: "Hoome sapiens"
//organisme: "Hoome sapiens"
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LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
LOCATION/Qualifiers
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Sequence 551 from Patent WO0073801.
AXO53785.
AXO53785.1 GI:12228104

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Sequence 559 from Patent WO0073801
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AX053793.1 GI:12228112
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Homo sapiens
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Best Local Similarity: 1
Query Match: 1
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Breast, gastric and prostate cancer associated antigens and uses therefor
Patent: W 0073801-A 560 07-DEC-2000;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
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Sequence 560 from Patent W00073801.
AX053794 AX053794.1 GI:12228113
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                 Breast, gastric and prostate cancer associated antigens and uses therefor
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                                              PATENT: WO 0073801-A 553 07-DEC-2000;
LUDWIG INSTITUTE FOR CANCER RESEARCH
LOCATION/QUALIFIERS
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Best Local Similarity: 1
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates, Catarrhini; Hominidae; Homo.
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Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of breast cancer
Patent: WO 0151628 A. 2910 197UL-2001;
Millennium Pharmaceuticals, Inc. (US)
                                                    1 MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla
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Sequence 553 from Patent WO0073801.
AX053787
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Sequence 2910 from Patent WO0151628.
CQ417876.1 GI:41370105

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Homo sapiens
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391 GAGAGTCTCTGT 402
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Job time : 669.152 secs
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Breast, gastric and prostate cancer associated antigens and uses
therefor
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Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer Patent: WO 0151628-A 12961 19-JUL-2001;

Millennium Pharmaceuticals, Inc. (US)

Location/Qualifiers

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LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
Location/Qualifiers
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Sequence 565 from Patent WO0073801.
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Homo sapiens
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382 GAGAGTCTCTGT 393
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Abc3322 Human tum
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Aaf22969 Human pro
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Ade4418 Human cDN
              Adn40408 Human bre
Acn92774 Breast ca
Acn87508 Breast ca
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Granados EN, Hodges SC, Klass MR, Kratochvil JD, Russell JC;
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AAA59008;
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Aal11595 Human bre
Aal16216 Human bre
Aal25059 Human bre
Aal20310 Human bre
                                                          August 1, 2005, 22:23:28; Search time 81.4834 Seconds (without alignments) 3196.585 Million cell updates/sec
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1 MQKSVPNKALELKNEQTLRA......PSESKQKDYEESSWDSESLC
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                           - nucleic search, using frame plus p2n model
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Claim 1; Page 740; 3695pp; English.
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                                                      Clones AAAS9007-13 were used to produce the full length and consensus sequences encoding BS322 polypeptide. BS322 is a breast tissue marker. The BS322 polymucleotides and polypeptides are used to detect and diagnose breast disease, e.g. breast cancer. The BS322 polymucleotides are useful as a source of probes and primers, and the BS322 polymucleotides are useful as antigens
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         used in
         BS322-specific polynucleotides, polypeptides and antibodies, used idetection and diagnosis of breast disease especially breast cancer
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                                                                                                                          62 G; 68 T; 0 U; 0 Other;
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                                       Claim 12; Fig 1A-E; 126pp; English
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14-MAR-2000; 2000US-0189167P.
24-MAR-2000; 2000US-0192099P.
29-MAR-2000; 2000US-0193480P.
15-MAY-2000; 2000US-0205230P.
09-UNA-2000; 2000US-0211315P.
25-JUL-2000; 2000US-0211315P.
                                                                                                                          Sequence 278 BP; 104 A; 44 C;
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The invention relates to human breast cancer expressed polymucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polymucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polymucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
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                                                                                                                                                                                                                                                                                     Sequence 445 BP; 153 A; 83 C; 98 G; 109 T; 0 U; 2 Other;
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14-MAR-2000; 2000US-0189167P.
24-MAR-2000; 2000US-019209P.
29-MAR-2000; 2000US-0193480P.
15-MAY-2000; 2000US-0205230P.
09-UUN-2000; 2000US-0211315P.
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      The invention relates to human breast cancer expressed polymucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polymucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polymucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
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The invention relates to human breast cancer expressed polymucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polymucleotides and encoded polymeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polymucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
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                                                                                                                                     Sequence 562
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(AALO7544-AAL26789) and methods of assessing whether a patient is a filiated with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                             AspGlulleLeuProSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSer
                                                                                                                                                                                                                                                                                           MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla
                                                                                                                                                                                                                                                                                                                      GATGAGATACTCCCATCAGAATCCAAACAAAGGACTATGAAGAAAGTTCTTGGGATTCT
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                                                                                                                          Sequence 572 BP; 137 A; 128 C; 109 G; 198 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human breast cancer expressed polynucleotide 12486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; breast cancer; cell marker; cytostatic; ss.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                               (1-572)
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                                                                                                                                                                                                                                                               US-09-489-079-26 (1-44) x AAL20310
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14-MAR-2000; 2000US-0189167P.
24-MAR-2000; 2000US-0199P.
25-MAR-2000; 2000US-0193480P.
15-MAY-2000; 2000US-0205230P.
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25-JUL-2000; 2000US-0220534P.
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                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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117 GATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAAAGTTCTTGGGATTCT 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a human breast tumour protein coding sequence. This sequence may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the breast tumour
afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
                                                                                                                                                                                                                                                                           MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla
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                                                                                                             Sequence 578 BP; 201 A; 112 C; 124 G; 141 T; 0 U; 0 Other;
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Matches:
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22-FEB-2000; 2000US-00510662.
10-MAR-2000; 2000US-00531886.
07-APR-2000; 2000US-00545068.
15-MAY-2000; 2000US-00571025.
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Best Local Similarity:
Query Match:
DB:
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and inhibiting the development of cancer.

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protein e.g. breast cancer. For example, this sequence may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of breast tumour protein by expressing inactive proteins or to supplement the patients own production of the breast tumour protein. Additionally, the present sequence may be used to produce the breast tumour protein, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The present sequence and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATGAGATACTCCCATCAGAATCCAAACAAAAGGACTATGAAGAAAGTTCTTGGGATTCT 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; breast cancer; T cell; tumour protein; antigen presenting cell; immune response; CD4+; CD8+; cytostatic; gene therapy; 88.
                                                                                                                                                                                                                                                                                                                                                                                MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                             AspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSer
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                                                                                                                                                                                        Sequence 580 BP; 139 A; 127 C; 112 G; 199 T; 0 U; 3 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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10-MAR-2000; 2000US-00523586.
07-APR-2000; 2000US-00545068.
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06-FEB-2001; 2001US-00778320
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Best Local Similarity:
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Mcneill PD;
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The present invention relates to polymucleotide and polypeptide sequences associated with breast cancer. Also disclosed are expression vectors comprising the polymucleotide sequences of the invention operably linked to an expression control sequence, host cells comprising the vector, antibodies (or antigen binding fragments of antibodies) specifically.

Comprising the polypeptides of the invention, fusion proteins comprising at least one of the polypeptides, stimulating and/or expanding T cells specific for a tumour protein. The polymucleotide sequences, polypeptide sequences, and antigen presenting cells can be administered therapeutically/prophylactically to induce an immune response. They can therefore the polymorphylactically to induce an immune response. They can be included with a physiological carrier/immunostimulant in compositions such as vaccines, particularly to treat or prevent cancers such as breast cancer. They can also be used to inhibit the development of cancer by incubating one or more of them with CD4+ and/or CD8+ T cells isolated from a patient, such that the T cells proliferate, and administering the proliferated T cells to the patient. The polymucleotide sequences are useful for detecting cancer in a patient. The polymucleotide sequence are producing T cell populations and antigen presenting cells. The present control of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      523 ATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAAAAATTGAGAGCA 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 580 BP; 139 A; 127 C; 112 G; 199 T; 0 U; 3 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                  SEQ ID NO 163; 151pp; English.
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Best Local Similarity:
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Pred. No.:
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                                    Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful an arker for breast cancer and in breast cancer therapy. Sequences given in records ACN798934 represent mucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
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                             Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
                                                                                                                                                                                                                     205 A; 108 C; 130 G; 136 T; 0 U; 21 Other;
                                                                                                                                                                                                     site at segdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                    Disclosure; SEQ ID NO 13924; 36pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer related marker, seq id 8658.
                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lillie J, Xu Y, Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                        US-09-489-079-26 (1-44) x ACN92774 (1-600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACN87508 standard; DNA; 635 BP.
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         WPI; 2003-787014/74
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Best Local Similarity:
                                                                                                                                                                                                                       Sequence 600 BP;
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DB:
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The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention are useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPFO web site at seqdata.uspto.gov/sequence.thml?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGAGATACTCCCATCAGAATCCAAAAAAGGACTATGAAGAAAGTTCTTGGGATTCT 497
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Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 635 BP; 213 A; 128 C; 154 G; 135 T; 0 U; 5 Other;
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99US-0153454P.
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Best Local Similarity:
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10-SEP-1999;
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                                                         cancer.
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AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate cancer associated antigen nucleotide sequence SEQ ID:559.
                                                                                                                                                                                                                                                                                                                                                                                                                    MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                 AspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSer
         Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     breast cancer; gastric cancer; prostate cancer; diagnosis; associated antigen; cytostatic; cancer vaccine; ss.
                                                                                                                                                                                                                                                      217 A; 120 C; 138 G; 157 T; 0 U; 4 Other;
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Matches:
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                                                                             Claim 50; Page 456; 799pp; English
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10-SEP-1999;
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cancer
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AAF22422 to AAF22656, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63468 to AAB63721 and AAB63722 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63370 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate cancer associated antigen nucleotide sequence SEQ ID:551.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla
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Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine; ss.
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                                                                       Claim 50; Page 455; 799pp; English
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                                                                                                                                                                                                                                                           Sequence 664
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                                               cancer.
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AAB63232 to AAB63467, AAB63468 to AAB63722 to AAB63722 to AAB63370 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
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  antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g
                                                                                                                                                                                                                                                                                                                                                       BP; 246 A; 134 C; 154 G; 172 T; 0 U; 2 Other;
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Matches:
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                                                                                   Claim 50; Page 453; 799pp; English.
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14-MAR-2000; 2000US-0189167P.
24-MAR-2000; 2000US-0192099P.
29-MAR-2000; 2000US-0193480P.
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                                                                                               The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspGlulleLeuProSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSer
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                                                                                                                                                                                                                                                                      polypeptides are also useful for isolating compounds with cytostatic activity
New peptide useful as a marker for the diagnosis of breast cancer
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cancer.

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AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63262 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                              Claim 50; Page 453-454; 799pp; English.
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Alignment Scores: Pred. No.: 225.00 Percent Similarity: 100.00\$ Matches: Percent Similarity: 100.00\$ Matches: Percent Similarity: 100.00\$ Matches: Percent Similarity: 100.00\$	713 44 tive: 0 es: 0
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US-09-489-079-26 (1-44) x AAF22974 (1-713)

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Search completed: August 1, 2005, 23:18:11 Job time: 85.4834 secs

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581 bp mRNA linear EST 17-SEP-2004 BB314867 Sugano cDNA library, mammary gland OCUB-F Homo sapiens EP314867
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Suzuki, Y., Yamaahita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
block structure in the promoter regions
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
1 Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-cokyo.ac.jp.
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E. (Dasses 1 to 582)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Department of Wirology
Institute of Medical Science, University of Tokyo
1-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysprauki@ims.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                              BP313026 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR01939, mRNA sequence.

BP313026.1 GI:52242001
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BP313436 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR03209, mRNA sequence.
BP313436 GI:52242411
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1 (bases 1 to 582)
2 (Bazuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Makai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuaki@ims.u-tokyo.ac.jp.
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BP313235.1 GI:52242210
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REPERENCE AUTHORS

TITLE

PEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 582)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Locatic translation (2004)

Contact: Yuralogy
Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzukishma.u-tokyo.ac.jp.
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BP314260 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR05703, mRNA sequence.
BP314260
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Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Dentact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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E 1 (bases 1 to 5812)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizuki, Y., Yamashita, R., Shirota, M., and Sugano, S. Geneco, Comparison of human and mouse genes reveals a homologous block structure in the promoter regions

L Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzukishma.u-tokyo.ac.jp.
                                                                                                                                                                                                                                              365
                                                                                           306 GATGAGATACTCCCATCAGAATCCAAAGAACTAATGAAGAAGTTCTTGGGATTCT 365
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583 bp mRNA linear EST 17-SEP-2004
BP313822 Sugano cDNA library, mammary gland OCUB-F Homo sapiens
BP313822
BP312890 583 bp mRNA linear EST 17-SEP-2004 BP312890 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR01356, mRNA sequence.
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Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
block structure in the promoter regions
connect: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-cokyo.ac.jp.
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Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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|/note="mammary gland tumor"
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41 GluSerLeuCys
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BP312910
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Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
L Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Institute of Wirology
Institute of Wedical Science, University of Tokyo
4-6-1, Shirokanedai, Minaloku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
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Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
1-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 584)
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Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Home sapiens

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 598)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

Institute of Medical Science, Tokyo 108-8639, Japan

Email: ysuzukiaAma.u-cokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP312910 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR01441, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                 260 ATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACAAAAAATTGAGAGCA 319
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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AUTHORS

DEFINITION

BF746270 LOCUS

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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                         BF746340 443 bp mRNA linear EST 10-JAN-2001
RC1-BT0254-081100-119-a03 BT0254 Homo sapiens CDNA, mRNA sequence.
BF746340
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Fax: +55-11-270001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-BT0254-
081100-119-a03&t5=2000-11-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 439.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
               21 AspGlulleLeuProSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSer
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1 (bases 1 to 443)

Dias Neto,E., Garcia Carca,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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Fax: +55-11-2707001

Fax: +55-11-2707001

Exact: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-BT0254-071100-119-a03&t3=2000-11-07&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 9

High quality sequence stop: 439.
                                                                                                                                                                                                                                                                                      BF746270 443 bp mRNA linear EST 10-JAN-2001 RC1-BT0254-071100-119-a03 BT0254 Homo sapiens cDNA, mRNA sequence.
                                                                         321 GATGAGATACTCCCATCAGAATCCAAACAACAACTATGAAGAAAGTTCTTGGGATTCT 380
40
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                AspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGluSerSerTrpAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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MEDLINE PUBMED COMMENT

FEATURES

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Score:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Bi (bases) 1 to 582)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizuki, M., Yamashita, R., and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block etructure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Wirology
Institute of Medical Science, University of Tokyo
1 Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
                             582 bp mRNA linear EST 17-SEP-2004
BP315089 Sugano cDNA library, mammary gland OCUB-F Homo sapiens
cDNA clone OFR07766, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla 20
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/cell_line="COUB-F"
/clone linesugano CDNA library, mammary gland OCUB-F"
/note="mammary gland tumor"
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93.18%
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Homo sapiens
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124 GACAGTCTCTGT 435
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Job time : 1677.51 secs
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AUTHORS
RESULT 15
BP315089
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
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/cell_line="COUB-F"
/clone_lib="Sugano CDNA library, mammary gland OCUB-F"
/note="mammary gland tumor"
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                                                                        MetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OFR04504"
       Gaps:
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Homo sapiens
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Aaf22981 Human pro
Aaf22980 Human pro
Aaf22972 Human pro
Aaf22974 Human pro
Aaf22996 Human pro
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Abs4419 Human bre
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Aa120310 Human bre
Aa120029 Human bre
Aan5538 Human bre
Adn40408 Human bre
Acn92774 Breast ca
Acn87508 Breast ca
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Abv28376 Human pro
Abv27350 Human pro
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Hodges SC, Klass MR, Kratochvil JD, Russell JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BS322; breast tissue marker; breast disease; breast cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of BS322 clone 4304443H1
                  AAL25059
AAL20310
AAL20310
AAL55638
ACN9274
ACN97508
AAF22981
AAF22991
AAF22991
AAF22991
AAF229969
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AAF17979
AAF17979
AAF47409
ABS44010
ABT3322
ADL93129
ADE4419
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ABV28376
ABV27350
ACN89282
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Granados EN, H
Stroupe SD;
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 AAA59008;
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Aal11595 Human bre
Abv13085 Human pro
Abv43067 Human pro
Abv34206 Human pro
                                                                        August 1, 2005, 22:23:28; Search time 70.372 Seconds (without alignments) 3196.585 Million cell updates/sec
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1 NKALELKNEGTLRADEILPSESKQKDYEESSWDSESLC 38
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                     - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                 hits satisfying chosen parameters:
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Listing first 45 summaries
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AAL11595
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Ygapop 10.0 , Ygapext
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Maximum DB seq length: 200000000
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                                                                                                                Clones AAA59007-13 were used to produce the full length and consensus sequences encoding BS122 polypeptide. BS122 is a breast tissue marker. The BS122 polynucleotides and polypeptides are used to detect and diagnose breast disease, e.g. breast cancer. The BS122 polynucleotides are useful as a source of probes and primers, and the BS122 polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                  BS322-specific polynucleotides, polypeptides and antibodies, used in the detection and diagnosis of breast disease especially breast cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          breast
                                                                                                                                                                                                                                                       Sequence 278 BP; 104 A; 44 C; 62 G; 68 T; 0 U; 0 Other;
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38
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Matches:
Conservative:
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                                                                             Claim 12; Fig 1A-E; 126pp; English.
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24-MAR-2000; 2000US-0192099P.
29-MAR-2000; 2000US-0193480P.
15-MAY-2000; 2000US-0205230P.
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Best Local Similarity:
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Query Match:
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; cytostatic; carcinogen; pharmacodyanamic marker;
marker; gene; 88.
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afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polymucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polymucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
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2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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Best Local Similarity:
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pharmacogenomic
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV65213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy
of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                             Sequence 466 BP; 171 A; 87 C; 104 G; 104 T; 0 U; 0 Other;
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2000US-0189862P.
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Best Local Similarity:
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25-MAY-2000;
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of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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Mismatches:
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25-WAY-2000; 2000US-0207454P.
09-UUN-2000; 2000US-021314P.
18-UUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
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pharmacogenomic marker;
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of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                              122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; cytostatic; carcinogen; pharmacodyanamic marker;
marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCys
                                                                                                                                                            Sequence 473 BP; 162 A; 91 C; 115 G; 105 T; 0 U; 0 Other;
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Matches:
Conservative:
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Indels:
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2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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pharmacogenomic
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16-MAR-2000;
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Pred. No.:
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of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                    58 AATAAAGCCTTGGAATTGAAGAATGAACAATTGAGAGCAGATGAGATACTCCCATCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human breast cancer expressed polymucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polymucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polymucleotides and encoded potentially preventing breast cancer. The polymucleotides and encoded
                                                                                                                                                                                                                                                                                                                                                                    AsniysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCys
                                                                                                                                                Sequence 508 BP; 176 A; 100 C; 120 G; 111 T; 0 U; 1 Other;
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338
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Matches:
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Mismatches:
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2000US-0192099P.
2000US-0193480P.
2000US-0205230P.
2000US-0211315P.
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Query Match:
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29-MAR-2000;
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Length: Matches: Conservative: Mismatches: Indels:

Gaps:

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Query Match Best Local

AAL25059

AAL25059 RESULT

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63 AATBAAGCCTTGGAATTGAAGAATGAACATTGAGAGCAGATGAGATGACTCCCATCA 122
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                                                                                                                                                                             1 AsnlysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer
                                                                                                                                                                                                                                                                                123 GAATCCAAACAAAAGGACTATGAAGAAAGTTCTTGGGATTCTGAGAGTCTCTGT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide useful as a marker for the diagnosis of breast cancer.
                                                                                                                                                                                                                                               21 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCys
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                                                                                                                                                                                                                                                                                                                                                        AAL20310 standard; cDNA; 572 BP
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15-MAY-2000; 2000US-0205230P.
26-JUL-2000; 2000US-0211315P.
25-JUL-2000; 2000US-0220534P.
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                                                                                                                                          US-09-489-079-27 (1-38)
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Best Local Similarity:
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 Alignment Scores:
Pred. No.:
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                                                                                        Query Match:
DB:
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polypeptides are also useful for isolating compounds with cytostatic activity
                                                                                                                                                                                                                                                                                                                                                                         145 GAATCCAAACAAAAGGACTATGAAGAAGTTCTTGGGATTCTGAGAGTCTCTGT 198
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                                                       0 U; 0 Other;
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                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                       C; 117 G; 122 T;
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2000US-0189167P.
2000US-0192099P.
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                                                       A; 106
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                                                       BP; 188
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                                                                                                                                                                  Similarity:
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                                                                                                                                            Percent Similarity:
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09-JUN-2000;
25-JUL-2000;
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                                                         Sequence 533
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24-MAR-2000;
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Length: Matches: Conservative: Mismatches:

AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer

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                                                                                         GAATCCAAACAAAAGGACTATGAAGAAAGTTCTTGGGATTCTGAGAGTCTGTGT 397
                                                                                                                                  GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCys 38
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                                             US-09-489-079-27 (1-38) x AAL20310 (1-572)
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14-MAR-2000; 2000US-0189L67P.
24-MAR-2000; 2000US-0193480P.
29-MAR-2000; 2000US-0193480P.
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09-JUN-2000; 2000US-0211315P.
25-JUL-2000; 2000US-0220534P.
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                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Pred. No.:
                                                                                                                                                                                                                                                                                       07-DEC-2001
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   Query Match:
DB:
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The present sequence is a human breast tumour protein coding sequence.

This sequence may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the breast tumour protein e.g. breast cancer. For example, this sequence may be used to treat disorders associated with decreased expression by rectifying treat tumour protein by expressing inactive proteins or deletions in a patient's genome that affect the activity of breast tumour protein by expressing inactive protein. Additionally, the present sequence may be used to produce the breast tumour protein, by inserting the nucleic acids into a host cell and culturing the cell to complementary sequences the protein. The present sequence and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy
encode them, useful
                                                                       188
                                            21 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCys 38
                                                                                                                                                                                                                                                         Cytostatic; vaccine; human; breast tumour protein; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ä,
                                                            Breast tumor polypeptides and the nucleic acids that encode t for the prevention, diagnosis and treatment of breast cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitcham JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580
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                                                                                                                                                                                                                             Human breast tumour protein clone 48970 DNA sequence.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                      BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-2000; 2000US-00510662.
10-NAR-2000; 2000US-0053586.
07-APR-2000; 2000US-00545068.
15-MAY-2000; 2000US-00571025.
                                                                                                                                                                                                                                                                                                                                                                                                 29-NOV-2000; 2000WO-US032520
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195.00
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                                                                                                                                      AAH55638 standard; DNA; 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-356154/37
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Best Local Similarity:
                                                                                                                                                                                                                                                                            gene therapy; ds
                                                                                                                                                                                                                                                                                                                                     WO200140269-A2.
                                                                                                                                                                                                                                                                                                          Homo sapiens
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                   07-JUN-2001
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                                                                                                                                                                    AAH55638;
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                                                                                                         RESULT 11
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US-09-489-079-27 (1-38) x AAH55638 (1-580)

578 38 0 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

5.19e-21 195.00 100.00% 100.00%

> Percent Similarity: Best Local Similarity: Query Match:

Gaps:

x AAL20029 (1-578)

US-09-489-079-27 (1-38)

Matches:

8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides, useful for treating and diagnosing cancer, particularly breast cancer by stimulating immune response in a patient and inhibiting the development of cancer.
                                                                                                                                                                                                                                             Human, breast cancer, T cell; tumour protein; antigen presenting cell;
immune response; CD4+; CD8+; cytostatic; gene therapy; ss.
 1 AsnlysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer
                                                                 21 GluSerLygGlnLygAspTyrGluGluSerSerTrpAspSerGluSerLeuCys 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitcham JL,
                                                                                                                                                                                                                     cancer associated cDNA sequence #160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 580 BP; 139 A; 127 C; 112 G; 199
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                                                                                                                                      ADN40408 standard; cDNA; 580 BP
                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1999; 99US-00451651.
22-FEB-2000; 2000US-00510662.
10-MAR-2000; 2000US-00523566.
17-APR-2000; 2000US-0054568.
15-MAY-2000; 2000US-00571025.
06-FEB-2001; 2001US-00778320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Day CH, Jiang Y,
                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2003; 2003US-00714389
                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-399689/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                  US2004101899-A1.
                                                                                                                                                                                                                     Human breast
                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                          12-AUG-2004
                                                                                                                                                                                                                                                                                                                                             27-MAY-2004
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Mcneill PD;
                                                                                                                                                                ADN40408;
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The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACNY8851.ACN9934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
                                                                                                                                                                                                       AsnlysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                                                                                                                                                                                                    Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
                                                                                                                                                                                                                                                                          21 GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCys 38
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                     Conservative:
Mismatches:
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                                                                   Indels:
                                                                                        Gaps:
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                                                                                                                                   x ADN40408 (1-580)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUL-2002; 2002US-00198846.
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                                                                                                                                      US-09-489-079-27 (1-38)
                     Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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DB:
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                                                                     Query Match:
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38

02-DEC-2004

Breast

ACN87508;

RESULT 14 ACN87508 ID ACN

셤 ઠ 엄 29-MAY-2003

Lillie J,

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AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and profester cancer associated antigen precursors (CAAP) respectively.

AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                  Human prostate cancer associated antigen nucleotide sequence SEQ ID:560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                   Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine; ss.
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Sequence 636 BP; 217 A; 120 C; 138 G; 157 T; 0 U; 4 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                   BP.
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                                                                                                                     AAF22981 standard; cDNA; 636
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                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                        AAF22981;
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DB:
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                                                                               RESULT 15
                                                                                                 AAF22981
ID AAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN79831-ACN9234 represent mucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
                                                                               513
                                           1 AsnlysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer 20
                                                                 Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                 Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at segdata.uspto.gov/sequence.html?DocID=20030099974
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                                                                                                                                                                                                                                                                                                                                                     cancer related marker, seg id 8658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steinmann K;
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     US-09-489-079-27 (1-38) x ACN92774 (1-600)
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                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003099974-A1
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Search completed: August 1, 2005, 23:18:12 Job time: 71.372 secs

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BD271305

Reagents and methods useful for detecting diseases of the breast.
BD271305

BD271305

JP 2002540761-A/2.
Homo sapiens (human)
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JP 2002540761-A/2
03-DEC-2002
21-JAC-2000 JP 2000594836
21-JAN-1999 US 09/224716
PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΡI
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1. (bases 1 to 278)
Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Russell,J.C. and Stroupe,S.D.
Reagents and methods useful for detecting diseases of the breast Patent: JP 2002540761-A 2 03-DEC-2002;
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JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R
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AR561591
AX282973
AX303146
AX367056
AR283468
AR454017
CC511219
CC6422641
CC6422641
CC6422463
CC6422463
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AXI563084
AXI563080
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BD271305
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   BD271305 Reagents
CQ419026 Sequence
CQ481209 Sequence
CQ502357 Sequence
                                                                                   August 1, 2005, 22:24:58; Search time 575.313 Seconds (without alignments) 3200.517 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 NKALELKNEQTLRADEILPSESKOKDYEESSWDSESLC 38
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                               nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                             4708233 segs, 24227607955 residues
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CQ502357
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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PAT 30-JAN-2004

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FEATURES

ORIGIN

Score:

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Schlegel, R., Endege, W.O. and Monahan, J.E.
Genes differentially expressed in human prostate cancer and their
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Genes differentially expressed in human prostate cancer and
            GluSerLysGlnLysAspTyrGluGluSerSerTrpAspSerGluSerLeuCys
                            117 GAATCCAAACAAAAGGACTATGAAGAAAGTTCTTGGGATTCTGAGAGTCTCTGT
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Mismatches:
Indels:
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                         Patent: WO 0160860-A 13076 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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                                                                                                     Sequence 13076 from Patent WO0160860.
CQ481209
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CQ502357
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                                             C12P21/02, C12Q1/68, G01N33/53, G01N33/53, G01N33/566, G01N33/574,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer.
Patent: WO 0151628-A 4060 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 AATAAAGCCTTGGAATTGAAGAATGAACAAACATTGAGAGCAGAGATGAGATACTCCCATCA
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C12N15/00,C12N5/00
Reagents and methods useful for detecting diseases of
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Location/Qualifiers
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Sequence 4060 from Patent WO0151628.
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lillie,J., Xu,Y., Wang,Y. and Steinmann,K.
Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer Patent: WO 0151628-A 8681 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Patent: WO 0160860-A 3907 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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Sequence 8681 from Patent WO0151628.
CQ423647
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/db_xref="taxon:9606"
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Homo sapiens
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Genes differentially expressed in human prostate cancer and their
use
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Genes differentially expressed in human prostate cancer and
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Millennium Predictive Medicine, Inc. (US)
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Sequence 43086 from Patent WO0160860.
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CQ511219.1 GI:41477483
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Sequence 3907 from Patent WO0160860.
CQ472041.1 GI:41437660

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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                             Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer Patent: WO 0151628 A 17529 19-ULL-2001;
Millennium Pharmaceuticals, Inc. (US)
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Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of breast cancer
Patent: WO 0151628-A 12778 19-UUL-2001,
Millennium Pharmaceuticals, Inc. (US)
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Compositions and methods for therapy and diagnosis of breast cancer Patent: WO 0140269-A 163 07-JUN-2001; CORIXA CORPORATION (US)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer Patent: WO 0151628-A 12497 19-JUL-2001; Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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CQ427463
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WO0140269.

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AX156306.1 GI:14537307
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PAT 13-JAN-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Breast, gastric and prostate cancer associated antigens and uses therefor Patent: WO 0073801-A 559 07-DEC-2000; LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
LOCATION/Qualifiers
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LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
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AXOS3785.1 GI:12228104

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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                       Breast, gastric and prostate cancer associated antigens and uses therefor
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                                                                                                                                               505 AATAAAGCCTTGGAATTGAAGATGAACAACATTGAGAGGGGGGTGAGTGCCCATCA
                                                                                                                                    1 AsniysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer
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Gaps:
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LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
Location/Qualifiers
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Sequence 560 from Patent WO0073801.
AXOS3794
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AX053793 664 bp
Sequence 559 from Patent W00073801.
AX055793
AX055793.1 GI:12228112
                                                                                                         (1-580)
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Homo sapiens
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Homo sapiens
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      Alignment Scores:
Pred. No.:
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RESULT 13

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PAT 28-JAN-2004
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                  iillie,J., Xu,Y., Wang,Y. and Steinmann,K.
Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer.
Patent: WO 015128-A 2910 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
1. .713
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Matches:
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    DNA
CQ417876 713 bp DN Sequence 2910 from Patent WO0151628. CQ417876 CQ417876.1 GI:41370105
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 1, 2005, 22:08:06; Search time 2.34123 Seconds (without alignments) 1561.672 Million cell updates/sec

US-09-489-079-27 195 1 NKALELKNEQTLRADEILPSESKQKDYEESSWDSESLC 38 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* **Датараве**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Describeron	hypothetical prote	flagellar biosynth	ein -	probable alpha hel	alpha	probable alpha hel	endospore developm	hypothetical prote	hypothetical prote		hypothetical prote	hypothetical prote	glutamyl-tRNA synt	hypothetical prote	kinesin-related pr	hypothetical prote	hypothetical prote	listeriolysin regu	G-box-binding prot	hypothetical prote	μ	•	hypothetical prote	5	hypothetical prote	hypothetical prote	major structural n	stringent response	starch synthase DU
•	ID		F83465		A85901	A49940	E91056	C40646	T47279		A47328		T32251	E83254	T15945	A55236	T25410	T46457	S34727	T12092	E85508	E90657	JN0602	G90592	T00587	G96585	T34154	VHXPLJ	G64230	T01265
	rength DB			752 2	_		237 2	332 2	173 2	396 2	1403 1	•	375 2	494 2	629 2	784 1	2331 2	139 2	237 2	257 2	616 2	616 2	697 2	876 2	1080 2	232 2	432 2	569 1	720 2	1674 2
	Match L	30.0	29.0	28.7	28.5	28.5	28.5	28.5	27.7	27.7	27.7	27.4	27.2	26.9	26.9	26.9	26.9	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.4	26.4	26.4	26.4	26.4
,	Score	58.5	56.5	99	55.5	55.5	55.5	55.5		54	54	53.5	53	52.5	52.5	52.5	52.5	52	52	52	52	25	52	52	52	51.5	51.5	51.5	51.5	51.5
Result	02	н	7	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

molybdate-binding molybdate-binding	hypothetical prote probable phosphosu	ammonium transport hypothetical prote	kinesin-related pr	reverse gyrase - T	ankyrin 1, erythro	ankyrin 1, erythro	ankyrin 1, erythro	N-acylamino acid r	Balbiani ring 1 pr	protein T12C24.12	myb-related protei	hypothetical prote
G90727 H85578	2 T06748 2 H72473	P82918	2 JC5831	2 C72409	2 B35049	2 A35049	L SJHUK	F69991	2 S24345	2 G86259	1 855095	2 S46754
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257	356 492	521	793	1104	1856	1880	1881	371	511	522	290	1226
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51 51	51	51	51	51	51	51	51	50.5	50.5	50.5	50.5	50.5
30	33 33	34	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Accession: T32483
R.Accession: T32483
R.A.Species: Caenorhabditis elegans
R.A.Species: Caenorhabditis elegans
C.Accession: T32483
R.A.Speciption: The sequence of C. elegans cosmid F52H2.
A.Reference number: Z21175
A.Accession: T32483
A.Access
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A;Introns: 53/3; 96/3; 132/3; 169/3; 249/2; 373/3; 638/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F52H2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 678;
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hypothetical protein F52H2.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 58.5; DE; Pred. No. 19; 4; Mismatches
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Best Local Similarity 50.0
Matches 15; Conservative
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flagellar biosynthesis protein FlhA PA1452 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C;Accession: F83465 F;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bachon, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim.; Lory, S.; Olson, M.V.

Altitle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83465
A;Accession: F83465
A;Accession: F83465
A;Residues: 1-707 <STO>
A;Coss-references: UNIPROT:Q913P9; GB:AE004574; GB:AE004091; NID:g9947391; PIDN:AAG048
A;Access-references: UNIPROT: G913P9; GB:AE004574; GB:AE004091; NID:g9947391; PIDN:AAG048
A;Coss-references: strain PA01
C;Genetics:
A;Genetics:
A;Genetic

us-09-489-079-27.rpr

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A;Cross-references: UNIPROT:P37328; GB:S67014; NID:9455660; PIDN:AAB28777.1; PID:9455661
A;Note: sequence extracted from NCB1 backbone (NCBIN:139978, NCBIP:139880)
A;Note: sequence extracted from NCB1 backbone (NCBIN:139978, NCBIP:139880)
A;Note: sequence extracted from NCB1 backbone (NCBIN:139978, NCBIP:139880)
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Bscherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: GB:AE000341, GB:U00096, NID:g1788899, PIDN:AAC75608.1; PID:g1788906, A,Experimental source: strain K-12, substrain MG1655
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RIMD 0509952
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                                                                                                                                                                                                                        probable alpha helix protein [imported] - Escherichia coli (strain K-12) c; Species: Escherichia coli (species: Escherichia coli (species: Bacherichia coli (species: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C; Accession: A49940; B65033
N. Liuu, J.; Magasanik, B.
J. Bacteriol. 175, 7441-7449, 1993
A; Title: The glnB region of the Escherichia coli chromosome.
A; Reference number: A49940; MuID:94042920; PMID:8226691
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32.6%; Pred. No. 14;
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Matches 14; Conservative
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Matches 14; Conserv
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A;Molecule type: DNA
A;Residues: 1-237 <LIU>
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C; Species: Bacherichia coli
C; Date: 16-Pb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C; Accession: A85901
R; Perna, N.T.; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; McTecrence number: A85480; MUID:21074935; PMID:11206551
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-237 <STO>
A; Cross-references: GB:AE005174; NID:g12516965; PIDN:AAG57669.1; GSPDB:GN00145; UWGP:238
A; Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable alpha helix protein yfhG [imported] - Bscherichia coli (strain O157:H7, substra
C;Species: Bscherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRI protein - yeast (Saccharomyces cerevisiae)
Alternate names: protein YD9302.14; protein YDR138w
Species: Saccharomyces cerevisiae
Date: 05-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
Accession: S51866; A34781
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                                        Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 752;
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                                        DB 2;
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332 NKAKQVAEQEVQRQQELLPAQRAQ-EVKELGWD 363
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Pred. No. 44;
3; Mismatches
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                                                                                                          9; Mismatches
                                    Score 56.5;
Pred. No. 36
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                                    29.0%;
33.3%;
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nes 15; Conservative
                                                                                                          11; Conservative
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Best Local Similarity
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natural killer cell tumor-recognition protein - human
NyAlternate names: cyclophilin-related NK-tumor recognition protein; natural killer-tum
C;Species: Homo appiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RiAnderson, S.K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortaldo, J.R. Proc. Natl. Acad. Sci. U.S.A. 90, 542-546, 1993
A;Title: A cyclophilin-related protein involved in the function of natural killer cells A;Reference number: A47328; MUID:93133824; PMID:8421688
A;Accession: A47328
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A;Residues: 1-1403 <AND>
A;Cross-references: UNIPROT:P30414; GB:L04288; NID:g181251; PIDN:AAA35734.1; PID:g18125
A;Experimental source: NK killer cells from adult blood
A;Note: sequence extracted from NCBI backbone (NCBIN:122798, NCBIP:122800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: UNIPROT: Q59072; GB: U67608; GB: L77117; NID: g1592245; PIDN: AAB99700.1
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C,Superfamily: natural killer cell tumor-recognition protein; cyclophilin homology
C,Keywords: alternative splicing; lymphocyte
F;60-230/Domain: cyclophilin homology <CYP>
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Length 173;
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                                                                                                                                                                    5 ELKNEQTLRADEILPSESKOKDYEESSWDSESLC 38
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   DB 2;
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                                                              5; Mismatches
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   Score 54; DB
Pred. No. 15;
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C; Superfamily: nifS protein
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Query Match 27.7%;
Best Local Similarity 38.2%;
Matches 13; Conservative
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Best Local Similarity
Matches 10; Conserv
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A, Gene: GDB: NKTR
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                                                                                                                      Cipacies: Bacillus subtilis
Cipacies: Bacillus subtilis
Cipacies: Bacillus subtilis
Cipace: 21-Sep-1993 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
A;Reference number: A40646; MUID: 93123172; PMID: 9419299
A;Reference number: A40646; MUID: 93123172; PMID: 9419299
A;Residues: 1-332 <ARAP
A;Residues: 1-322 <ARAP
A;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T47279
R;Nyakatura, G:; Fartmann, B:; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24458
A;Accession: T47279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14766.1; PID:e1184055
A;Experimental source: strain 168
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C;Superfamily: Arabidopsis thaliana hypothetical protein P26B15.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.5%; Score 55.5; DB 2; Length 332; Best Local Similarity 30.6%; Pred. No. 20; Matches 11; Conservative 11; Mismatches 13; Indels
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A;Experimental source: cultivar Columbia; BAC clone F26B15
                                                                     endospore development protein spoIIB - Bacillus subtilis N;Alternate names: stage II sporulation protein spoIIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: H69710
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A,Gene: spo118
C,Keywords: sporulation; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-332 < KUN>
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A,Molecule type: DNA
A,Residues: 1-173 <NYA>
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: ONIPROT: Q9XCL6; GB: AE004737; GB: AE004091; NID: G9949239; PIDN: AAG0652
A; Experimental source: strain PAO1
A; Genetics:
A; Genetics:
C; Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-629 «MIL»
A;Cross-references: UNIPROT:Q19086; EMBL:U13070; NID:g529697; PID:g529702; PIDN:AAC46639
A;Experimental source: strain Bristol N2
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N.Alternate names: kinesin-like protein 5; KLP5
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Accession: A55236; E41298
R;Pesavento, P.A.; Stewart, R.J.; Goldstein, L.S.B.
J. Call Biol. 127, 1041-1048, 1994
A;Title: Characterization of the KLP68D kinesin-like protein in Drosophila: possible rol. A;Reference number: A55236; MuID:95050960; PMID:7525600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: mRNA
A,Residues: 1-794 < PBS.
A,Residues: 1-794 < PBS.
A,Cross-references: UNIPROT: P46867; GB:U15974; NID:G595912; PIDN:AAA69929.1; PID:G565090
R,Stewart, R.J.; Pesavento, P.A.; Woerpel, D.N.; Goldstein, L.S.B.
R,Stewart, R.J.; Pesavento, P.A.; Woerpel, D.N.; Goldstein, L.S.B.
R,Stewart, R.J.; Pesavento, P.A.; Woerpel, D.N.; Goldstein, L.S.B.
A,Title: Identification and partial characterization of six members of the kinesin super
A,Reference number: A41298; MUID:92020874; PMID:1924306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cispecies: Caenorhabdatis elegans
Cispecies: Caenorhabdatis elegans
Cispecies: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
Cispeciession: T15945
Similar, N
submitted to the EMBL Data Library, July 1995
Airescription: The sequence of C. elegans cosmid F01F1.
Airecence number: 218435
Airecession: T15945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
*Kesidues: 'TC',222-337,'VRGQV' <STE>
A;Cross-references: GB:M74431; NID:g157791; PIDN:AAA28658.1; PID:g157792
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: CESP:F01F1.5
A,Introns: 120/2; 286/3; 384/1; 478/2
C,Superfamily: Synechocystis hypothetical protein slr0825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 KGGESSNEVTLK----DGTGKQINYSEPTWDGDEL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.9%; Score 52.5; DB 2; 36.1%; Pred. No. 1e+02; tive 4; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F01F1.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                            5
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                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                         Score 52.5; D
Pred. No. 76;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               || :| || | | || || 212 LRGEEWLPSAPKLIKLYEYFGWEQPQLC 239
                                                                                                                                                                                                                                                                                                                                                                                                                       12 LRADELLPSESKO-KDYEESSWDSESLC 38
                                                                                                                                                                                                                                                                                         ch 26.9%;
1 Similarity 46.4%;
13; Conservative 5
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nes 13; Conservative
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Best Local Similarity
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                                                                                                hypothetical protein F3A4.240 - Arabidopsis thaliana
(;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T45869
R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23007
A;Accession: T45869
A;Accession: T45869
A;Accession: T45869
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-511 <BAR>
A;Cross-references: UNIPROT:Q9SN02; EMBL:AL132978
A;Experimental source: cultivar Columbia; BAC clone F3A4
C;Genetics:
C;Genetics:
A;Motp position: 3
A;Mote: F3A4.240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T15B7.15 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32251
R;Pauley, A; Gattung, S.
R;Pauley, A, Gattung, S.
R;Reference number: Z21139
A;Reference number: Z21139
A;Reference number: Z21139
A;Residues: 1-375 <PAU>A;Residues: 1-375 <PAU>A;Residues: 1-375 <PAU>A;Residues: UNIPROT:017039; EMBL:AF022985; PIDN:AAB69968.1; GSPDB:GN00023; CESP:C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholy. A;Reference number: A82950; MUID:20437337; PMID:10984043
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Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Accession: B83254
                                                                                            Pothetical protein F3A4.240 - Arabidopsis thaliana
Species: Arabidopsis thaliana (mouse-ear cress)
Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ALELKNEQTLRADEILPSESKOK---DYEESSWDSESLC 38
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A;Introns: 22/3; 63/3; 111/1; 162/2; 252/3; 288/3; 339/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches 13;
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Pred. No. 59;
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Best Local Similarity 38.55
Matches 15; Conservative
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Gaps

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Indels

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A;Gene: FlyBase:Klp68D; KLP5
A;Cross-references: FlyBase:FBgn0004381
A;Cross-references: FlyBase:FBgn0004381
A;Cross-references: FlyBase:FBgn0004381
A;Description: may be part of a motor protein that provides anterograde fast axonal tranc;Superfamily: kinesin-related protein KIF3; kinesin motor domain homology
C;Keywords: ATP; coiled coil; microtubule binding; nucleotide binding; P-loop
F;10-349/Domain: kinesin motor domain homology ckWOT>
F;10-313/Region: nucleotide-binding motif A (P-loop)
F;10-113/Region: nucleotide-binding motif A (P-loop)
F;581-784/Domain: helical rod #status predicted ckOD>
F;581-784/Domain: tail globular #status predicted ckOD>
F;112/Binding site: ATP (Lys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.9%; Score 52.5; DB 1; Length 784; Best Local Similarity 41.9%; Pred. No. 1.3e+02; Matches 13; Conservative 5; Mismatches 12; Indels
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Search completed: August 1, 2005, 22:23:20 Job time: 4.34123 secs

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581 bp mRNA linear EST 17-SEP-2004 BP314867 Sugano cDNA library, mammary gland OCUB-F Homo saplens cDNA clone OFR07276, mRNA sequence.
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78 PCL2374 M
33 RC1-BT025
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G084P07.5
G084P07Y
AU132223
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BP312630
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BP349185
                                                                   wx63g05.x
Homo Bapi
RC5-BN019
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RPCI-23-4
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CR735535
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Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
block structure in the promoter regions
Contact: Yutaka Suzuki
Department of Virology
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ISB1-50B1
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AGENCOURT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AV835394
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CL108568
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AC213306
CC313306
CR725535
BQ429618
AQ90800
AV835394
CN841887
CK603996
                                                                                                                                                                                     CK102592 (BI128959 (AU132223 CR627244 BP312630 CN787741 BP349185 I
                                                     A1951118
BC028407
BF328582
AO546028
AQ423531
AZ576125
AZ576125
BF171278
BE062233
BU811432
                                 BF746340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                            BP313800
BP315089
AI951118
BC028407
BP328582
AQ546028
AQ423531
AZ576125
HSMC18H11
                                                                                                                                                                                     CK102592

M112859

AU132223

CK627244

BP112630

CN787741

BP349185

BF179023

CL109041

CL108568

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AZ110334

HSM601761

CE313306

CR735535

BQ429618

AQ090800

AV855394

CK633996

CK1841887
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Homo sapiens
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KEYWORDS
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AUTHORS
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BP314867
LOCUS
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-MODEL=frame+ p2n.model -DEV=Xlp
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-ODGOLLIGN=200 -THR_SCORE=pct -THR_MAX=100 -TMR_NIN=0 -ALIGN=15 -MODE=LOCAL
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BP315806
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BP313822
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BP313436
BP313704
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1 NKALELKNEQTURADEILPSESKQKDYEESSWDSESLC 38
              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                            - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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9b_est2::
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9b_est6:::
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BP313235.1 GI:52242210
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Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homa sapiens

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 582)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

L Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzukiaina.-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                      BP313026 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR01939, mRNA sequence.

BP313026 I GI:52242001
                                                                                                                                                                        61 AATAAAGCCTTGGAATTGAAGAATGAACAATGAGACATTGAGAGCAGATGAGATTGATCCCCATCA 120
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/clone lib="Sugano cDNA library, mammary gland OCUB-F"
/note="mammary gland tumor"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
El (Dases 1 to 582)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizukiima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
1-6-1, Shirokanedai, Minatcku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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BP313235 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR02569, mRNA sequence.
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous Genome Res. 14 (9), 1711-1718 (2004)
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/cissue_type="mammary gland"
/cissue_line="course"
/cissue_line="Sugano cDNA library, mammary gland OCUB-F"
/note="mammary gland tumor"
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Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 582)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Contact: Yutaka Suzuki
Department of Virology
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzukiakima.u-cokyo.ac.jp.
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BP315806 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR09418, mRNA sequence.
BP315806
BP315806.1 GI:52244781
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Buaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

B 1 (Dases 1 to 582)

S Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

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block structure in the promoter regions

L Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

1-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp.
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/note="mammary gland tumor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-cokyo.ac.jp.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Homo sapiens
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db xref="taxon:9606"

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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 583)
S Suzuki,Y.: Yamashita,R.: Shirota,M.; Sakakibara,Y.; Chiba,J.;
Mizushima-Sugano,J.; Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

L Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 582)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizuki, Y., Yamashita, R., and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

L Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yeuzukielma: u-tokyo.ac.jp.
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/mol_type="mRNA"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
Bar (bases 1 to 583)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizukhima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Contact: Yutaka Suzuki
Department of Virology
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukiaina: u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP313822 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR04566, mRNA sequence.
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us-09-489-079-27.rst

DEFINITION

RESULT 10 BP314652

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AUTHORS REFERENCE

TITLE

ACCESSION VERSION KEYWORDS SOURCE

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1 (bases 1 to 443)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Coste, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-BT0254-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF746270 443 bp mRNA linear EST 10-JAN-2001
RC1-BT0254-071100-119-a03 BT0254 Homo sapiens cDNA, mRNA sequence.
BF746270
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                          reveals a homologous
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Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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BP312910
BP312910.1 GI:52241885
BP312910.1 GI:52241885
                                                                                                                                                                              17-SEP-2004
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Contact: Yutaka Suzuki
Department of Virology
Institute of Madical Science, University of Tokyo
1. Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
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          233 AATAAAGCCTTGGAATTGAAGAATGAACAAACGTTGAGAGCAGATGAGATACTCCCATCA 292
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1 (bases 1 to 598)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 584)
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High quality sequence start: 9
High quality sequence stop: 439-
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF746340 aRNA linear EST 10-JAN-2001 RCI-BI0254-081100-119-a03 BT0254 Homo sapiens cDNA, mRNA sequence.
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Bmail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BT0254-081100-119-a03&t3=2000-11.08&t4=1)
                                                                                                                                                                                                              /mol type="mana" | //mol t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AsnLysAlaLeuGluLeuLysAsnGluGlnThrLeuArgAlaAspGluIleLeuProSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 GAATCCAAACAAAAGGACTATGAAGAAAGTTCTGGGGATTCTGAGAGTCTCTGT 309
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Mismatches:
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Matches:
071100-119-a03&t3=2000-11-07&t4=1)
Seg primer: puc 18 forward
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High quality sequence stcp: 439.
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                                                                                                                                                                                           /organism="Homo sapiens"
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583 bp mRNA linear EST 17-SEP-2004 BP313800 Sugano cDNA library, mammary gland OCUB-F Homo sapiens CDNA clone OFR04504, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Justicy T. Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Genome Res. 14 (9), 1711-1718 (2004)
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 583)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Bu (Dases 1 to 582)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizukinima. Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
L Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minacku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                 BP315089 582 bp mRNA linear BST 17-SEP-2004 BP315089 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR07766, mRNA sequence.
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/cell_line="COUB-F"
/clone_lib="Sugano CDNA library, mammary gland OCUB-F"
/note="mammary gland tumor"
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Homo sapiens
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Search completed: August 2, 2005, 11:46:13 Job time : 1447.31 secs

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August 1, 2005, 22:04:01; Search time 13.5071 Seconds (without alignments) 1088.086 Million cell updates/sec
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1 NKALBLKONEQTLRADEILPSESKQKDYEESSWDSESLC 38
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	aci	aci	pro	bre	pro	aci	bre	spl	bre	bre	tum	pre	bre	bre	spl										
ű	Amino	Amino	Human	Human	Human	Human	Human	Нишап	Human	Amino	Human	B726P	Human	Human	Human	Human	Human	Human	B726P						
Description	Aab07641	Aab07640	Aab63909	Aab63906	Aab63926	Aab63933	Aab63929	Aab63918	Aab63937	Aab63917	Aab63903	Aab63901	Aab63925	Adb83983	Aab63899	Aab07638	Aab50249	Aag65987	Aau33350	Abg78917	Abj37740	Ad193135	Ade44425	Aab50248	Aag65986
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e E	AAB07641	AAB07640	AAB63909	AAB63906	AAB63926	AAB6393.	AAB63929	AAB63918	AAB63937	AAB63917	AAB63903	AAB63901	AAB63925	ADB83983	AAB63899	AAB07638	AAB50249	AAG65987	AAU33350	ABG78917	ABJ3774	ADL93135	ADE44425	AAB50248	AAG65986
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Query Match	100.0	-	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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4 AAU33349 5 5 ABG78916	901	~ 60	4 AAB84701	4	4	4	Ŋ	9	7	80	9	7	4	3 5 ABG78925	3 6 ABJ37748	3 7 ADL93156	2 4 AAU33351
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26 195	28 195	30 195	31 195	32 195	33 195	34 195	35 195	36 195	37 195	38 195	39 195	40 195	41 195	42 195	43 195	44 195	45 195

ALIGNMENTS

The present sequence represents an antigenic peptide derived from human BS322 polypeptide. The peptide is used to raise antibodies. BS322 is a breast tissue marker. The BS322 polymucleotides and polypeptides are used to detect and diagnose breast disease, e.g. breast cancer. The BS322 polymucleotides are useful as a source of probes and primers, and the BS322 polypeptides are useful as antigens BS322-specific polynucleotides, polypeptides and antibodies, used in the detection and diagnosis of breast disease especially breast cancer. Amino acid sequence of an antigenic peptide from BS322 polypeptide. Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J; Granados EN, Hodges SC, Klass MR, Kratochvil JD, Russell JC; Stroupe SD; BS322; breast tissue marker; breast disease; breast cancer Claim 23; Page 125; 126pp; English. AAB07641 standard; peptide; 38 AA. 99US-00234716. 21-JAN-2000; 2000WO-US001452 (first entry) WPI; 2000-499217/44. (ABBO) ABBOTT LAB Sequence 38 AA; WO200043420-A1. Homo sapiens. 07-NOV-2000 21-JAN-1999; 27-JUL-2000. AAB07641;

Gaps ö Query Match 100.0%; Score 195; DB 3; Length 38; Best Local Similarity 100.0%; Pred. No. 4.4e-19; Matches 38; Conservative 0; Mismatches 0; Indels

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RESULT

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represent nuclectide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63122 to AAB63122 to AAB63122 to AAB63722 to AAB63722 to AAB63722 to AAB63722 to AAB6370 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, spetides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate cancer associated antigen protein sequence SEQ ID NO:1268.
                                                                                                                                                                                                                                                                      Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                    AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
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                                                                                                                                                              (LUDW-) LUDWIG INST CANCER RES
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99US-0153454P.
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                                                                                                                                                                                                                                      WPI; 2001-025274/03.
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Best Local Similarity
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WO200073801-A2
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                                                                       26-MAY-2000;
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10-SEP-1999;
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10-SEP-1999;
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                                                                                                                                                                                                    Obata Y;
                                                                                                                                                                                                                                                                                                                                  cancer.
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Matches
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                                                                                                                                                                                                                                        Amino acid sequence of an antigenic peptide from BS322 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gordon J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast cancer; gastric cancer; prostate cancer; diagnosis; associated antigen; cytostatic; cancer vaccine.
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chvil JD, Russell JC;
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                                                                                                                                                                                                                                                                          BS322; breast tissue marker; breast disease; breast cancer
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                      1 NKALELKNEQTLRADEILPSESKOKDYEESSWDSESLC 38
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100.0%; Pred. No. 5.3e-19;
ive 0; Mismatches 0;
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                                                                                                                              AAB07640 standard; peptide; 44
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Hodges SC,
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Best Local Similarity 100.
Matches 38; Conservative
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RESULT 3 AAB63909

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Gaps

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e.g. cancer
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represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63232 to AAB63468 to AAB63468 to AAB63721 and AAB63722 to AAB63467.

AB62323 to AAB63468 to AAB63468 to AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein, Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g. Query Match
Best Local Similarity 100.0%; Score 195; DB 4; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 38; Conservative 0; Mismatches 0; Indels (Example 1; Page 770-771; 799pp; English Sequence 169 AA;

1 NKALELKNEQTLRADEILPSESKOKDYEESSWDSESLC 38 셤 8

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Gaps

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AAB63926 standard; protein; 174 AAB63926; RESULT 5 AAB63926

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26-MAR-2001

Human prostate cancer associated antigen protein sequence SEQ ID NO:1288. (first entry)

Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.

Homo sapiens

WO200073801-A2

07-DEC-2000

26-MAY-2000; 2000WO-US014749

99US-0136526P 99US-0153454P. 28-MAY-1999; 10-SEP-1999; (LUDW-) LUDWIG INST CANCER RES.

Obata Y;

WPI; 2001-025274/03.

Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g. cancer.

Example 1; Page 779; 799pp; English.

AAF22422 to AAF22626, AAF22677 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63232 to AAB63721 and AAB63722 to AAB6370 and breast, gastric and prostate CAAP protein sequence respectively. CAAP9 have cytostatic activity and can be used in the

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production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
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100.0%; Pred. No. 3.2e-18;
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100.0%; Pred. No. 3e-18;
tive 0; Mismatches 0;
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99US-0153454P.
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es 38; Conserv
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                                                     e.g. cancer
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Matches
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RESULT 7

AAB63929

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represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63232 to AAB63467, AAB63468 to AAB63701 and AAB63722 to AAB63970 respectively.

CAAP8 have cytostate CAAP protein sequence respectively. CAAP8 have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
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100.0%; Pred. No. 3.5e-18;
ive 0; Mismatches 0;
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99US-0153454P.
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Les 38, Conserv
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                                                      WO200073801-A2.
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                Homo sapiens.
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10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                          cancer.
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Matches
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                                                                                                                                                                                            Human prostate cancer associated antigen protein sequence SEQ ID NO:1291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate cancer associated antigen protein sequence SEQ ID NO:1280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                              breast cancer; gastric cancer; prostate cancer; diagnosis; associated antigen; cytostatic; cancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 195; DB 4;
100.0%; Pred. No. 3.3e-18;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 780; 799pp; English.
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                                                                        AAB63929 standard; protein; 189 AA.
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99US-0153454P.
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1es 38; Conservative
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                                                                                                                                                                                                                                  Human; breast
                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                           Homo sapiens
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Best Loc Matches

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Gaps

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Length 195; Indels

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26-MAY-2000; 2000WO-US014749
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Best Local Similarity 100.
Matches 38; Conservative
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Best Local Similarity
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10-SEP-1999;
                                                                      e.g. cancer
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate cancer associated antigen protein sequence SEQ ID NO:1279.
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                                              Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                        Example 1; Page 783-784; 799pp; English.
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                         WPI; 2001-025274/03.
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  Obata Y;
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                                                                                    cancer.
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AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
AAB63332 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
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                                                                                                                                                                                                                                                                                                                                                                                        4; Length 220;
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100.0%; Pred. No. 4e-18;
ive 0; Mismatches 0; Indels
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1 Similarity 100.0%; Pred. No. 4.1e-18;
38; Conservative 0; Mismatches 0;
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AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
              Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
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100.0%; Pred. No. 4.2e-18.
ive 0; Mismatches 0.
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Matches 38; Conservative
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10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate cancer associated antigen protein sequence SEQ ID NO:1287.
                                                                                                                                                                                                                                                              Human prostate cancer associated antigen protein sequence SEQ ID NO:1263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                  Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
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                   104 NKALELKNEQTLRADEILPSESKQKDYEESSWDSESLC 141
1 NKALELKNEQTLRADEILPSESKOKDYEESSWDSESLC 38
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100.0%; Pred. No. 4.1e-18;
ive 0; Mismatches 0;
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99US-0153454P.
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Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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10-SEP-1999;
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AAF22422 to AAF22656, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63468 to AAB63701 and AAB63722 to AAB63467, AB63468 to AAB63701 and AAB63722 to AAB63407 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPS have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                           Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                  28 NKALELKNEQTLRADEILPSESKQKOYEESSWDSESIC 65
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Best Local Similarity 100.
WPI; 2001-025274/03.
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                                                                             cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                              The invention related to a combination of polynucleotides. The combination of polynucleotides is useful for preparing a composition for diagnosimg or treating cancer or neurodegenerative disorders. The present sequence represents the amino acid sequence of the human breast cancer diagnostic marker Incyte 411152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate cancer associated antigen protein sequence SEQ ID NO:1261.
                                                                                                                                                                                                                                                                                                                                                       combination of polynucleotides, useful for preparing a composition diagnosing or treating cancer or neurodegenerative disorders.
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                                                               /note= "Encoded by AGA"
   /note= "Encoded by TTT"
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Matches 38; Conservative
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(MAHI/) MAHINI B.
(WALK/) WALKER M G.
                    Misc-difference 83
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                                                 Misc-difference
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10-SEP-1999;
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Length 266; Indels

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195
1 NKALELKNEQTLRADEILPSESKQKDYEESSWDSESLC 38
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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YFHG ECOLI SP2B_BACSU Q7mA44 Q7mA44 O56966 Q7RHR7 Q7RHR7 Q7RHR7 Q1EPR9 Q1EPR9 Q79LN3 Q79LN3 Q79LN3 Q79LN3 Q79LN3	ALIGNMENTS PRT; 1341 AA. Created) Last sequence update) Last annotation update) R-1. ta; Craniata; Vertebrata; Eutel	1280766; are A.O., Scanlan M.J., I.J., Chen Y.T.; e-specific Putative Transal Screening of a Breast of 1. NAS. NAS. binding; NAS. ption factor activity; NJ on of transcription, DNA, ASP_AS. AT, 4. REGION; 1. REGION; 1.	1341 AA; 152776 MW; 33ESSDDESFUSASES CACCE; imilarity (100.0%; Score 195; DB 2; Length ; Conservative (); Mismatches (); Indels NKALELKNEGTLRADEILPSESKOKDYEESSWDSESLC 38	PRT; 1011 AA. , Created) , Last sequence update) , Last annotation update R-1.1 (Fragment).
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Query Match
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MEDLINE=21174979; PubMed=11280766;
A Jaeger D., Stockert E., Guere A.O., Scanlan M.J., Karbach J.,
Jaeger D., Stockert E., Guere A.O.,
Jaeger E., Knuth A., Old L.J., Chen Y.T.;
T. Identification of a Tissue-specific Putative Transcription Factor in
Breast Tissue by Serological Screening of a Breast Cancer Library.";
Cancer Res. 61:2055-2061(2001).
R EMBL; AF559088; AAK27326.1; -.
R INCEPPO, IPR002110; ANK.
R Pfam; PF00023; Ank; 3.
R SMART; SM00248; ANK; 3.
R PROSITE; PS50088; ANK REPEAT; 1.
R PROSITE; PS50089; ANK REPEAT; 1.
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EMBL; Ali36793; CAB66727.1; -.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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1011 AA; 114250 MW; 16627D7B218DE438 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp434A171.
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Pred. No. 1.2e-09;
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PROSITE; PS50297; ANK REP REGION; 1.
ANK repeat; Hypothetical protein.
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78.9%;
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TISSUE=Testis;
The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 18.93
Best Local Similarity 78.93
Matches 30; Conservative
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SMART; SM00248; ANK; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002110; ANK. Pfam; PF00023; Ank; 6.
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                           NCBI_TaxID=9606;
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RESULT 090ZW8

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=Testis;
MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Bnzymol. 303:19-44(1999).
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
11brary, clone:4930483N21 product:similar to DNAJ-LIKE PROTEIN.
Name=4930503B20Rik;
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STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-Wistar; TISSUE-Testis;
Wang L., Miao S., Yang J., Zhang X., Zhao M., Li M.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFIS4849; AAD53061.1;
HSSP; P25685; 1HDJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 AA; 25756 MW; EBB4ADFC3CC92D3F CRC64;
                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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223 AA
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Pred. No. 21;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KALELKNEQTLRADEILPSESKOKDYEESSW 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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STRAIN=C57BL/6J; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IRR001623; DnaJ N. Pfam; PF00226; DnaJ; 1. SWART; SM00271; DnaJ; 1. PROSITE; PS0076; DNAJ 1; 1. PROSITE; PS0076; DNAJ 2; 1. SEQUENCE 223 AA; 25756 MW;
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41.9%;
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                                                                                                                                                                          Dnaj-like protein.
Rattus norvegicus (Rat).
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PRELIMINARY;
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TISSUE=Testis;
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Q811E2;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

A Arakawa T., Arzanaci P., Fukuda S., Fukunishi Y., Anno H.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Hanagaki T., Hara A., Hayatsu N., Hiramcto K., Hiraoka T., Hori F.,

A Kawai J., Kojima Y., Konno H., Izawa M., Koya S., Kurihara C.,

A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

Okazaki Y., Okido T., Owa C., Saito R., Sakai C., Sakai K.,

A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.,

Submitted (JUU-2000) to the EMBL/GenBank/DDBJ databases.
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feringold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Testie;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramereu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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226 AA; 25977 MW; A22055BBC8694599 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 31.3%; Score 61; DB 2; Local Similarity 40.6%; Pred. No. 28; les 13; Conservative 5; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KALELKNEQTLRADEILPSESKOKDYEESSWD 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005739; C:mitochondrion; IDA.
InterPro; IPR001623; DnaJ.N.
Pfam; PP00226; DnaJ; 1.
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01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
4930503820Rik protein.
Name=4930503820Rik;
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PROSITE; PS50076; DNAJ
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Matches
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Soarea M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Reha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

""" "Generation and initial analysis of more than 15,000 full-length human
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Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 31.3%; Score 61; DB 2; Length 234; Best Local Similarity 40.6%; Pred. No. 29; Matches 13; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 851 AA; 101937 MW; 466174BC463FD823 CRC64;
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PROSITE; PS50076; DNAJ 2; 1.
SEQUENCE 234 AA; 26907 MW; C2E8D7EEB71AFC9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.3%; Score 61; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KALELKNEQTLRADEILPSESKQKDYEESSWD 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 BAAEEKFKQVAEAYHILSDAKKRKDYDRSRWN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      851 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005739; C:mitochondrion;
InterPro; IPR001623; DnaJ N.
Pfam; PF00226; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1922264; 4930503B20Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE014839; AAN35816.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC048658; AAH48658.1;
HSSP; P25685; 1HDJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Myxococcus xanthus.
                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                         OBKRC9
                                                                                                                                                                                                                                                                                                                                                                              OBKRC9
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Q8KRC9
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             Gaps
                                                                                                                                                                                Name=T7M13.23;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                            GO:0005694; C:chromosome; IEA.
GO:0005524; F:ATP binding; IEA.
GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
GO:0006265; P:DNA topological change; IEA.
GO:0006268; P:DNA unwinding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Library Benito M., Creasy T.H., Haas B.J., Wu Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
                                                                                                                                                                                                                                                                            M B.,
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas
Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO11708; AAF19580.1; --
HSSP; P09097; LAB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 899;
           13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00434; TOP4c; 1.
TIGRFAMB; TIGR01063; GyrA; 1.
SEQUENCE 899 AA; 99547 MW; 1AC44F32B36E8333 CRC64;
                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Putative DNA gyrase A subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative DNA gyrase subunit A; 1114-7603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 60.5; DB 2;
Pred. No. 1.5e+02;
37.5%; Pred. No. 1.2e+02;
tive 7; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KALELKNEQTLRADEILPSESKQKDYEESSWD 33
                                               10 KGLETKNETIIEKENKEVEEEKEKEFEESEYN 41
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43.8%; Pred. No. 1...
8; Mismatches
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                                                                                                              899 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               917 AA
                                                                                                                                    (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IRR005743; DNA_gyrA.
InterPro; IRR006691; DNA_gyraseA_C.
InterPro; IPR00205; DNA_topoisoIV.
Pfam; PF03899; DNA_topoisoIV, I.
ProDom; PD000742; DNA_topoisoIV; I.
                                                                                                              PRT;
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Best Local Similarity 43.89
          12; Conservative
                                                                                                               PRELIMINARY;
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 Best Local Similarity
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                                                                                                                                    01-MAY-2000
                                                                                                              09SG75
09SG75;
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Q9CAF6;
             Matches
                                                                                       RESULT 8
Q9SG75
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
the ATPase activity of dnak (By similarity).
-!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the dnaJ family.
-!- SIMILARITY: Belongs to the dnaJ family.
-!- SIMILARITY: Belongs to the HasP; P25685; 1HDJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                          SEQUENCE FROM N.A.
Town C.D., Kaul S.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ACOLISEO; AAG51377.1; -.
HSSP; P09097; 1AB4.
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0051082; F:unfolded protein binding; IEA.
GO; GO:0006260; P:DNA replication; IEA.
GO; GO:0006457; P:protein folding; IEA.
GO; GO:000696; P:response to unfolded protein; IEA.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.0%; Score 60.5; DB 2;
43.8%; Pred. No. 1.5e+02;
ive 8; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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InterPro; IPR001305; DnaJ.C.
InterPro; IPR001623; DnaJ. CXXCXGXG.
InterPro; IPR001623; HSP40 DnaJ.pep.
InterPro; IPR003095; HSp_DnaJ.
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Pfam; PP0155; DnaJ C; 1.
Pfam; PP00155; DnaJ C; 1.
SMART; SW00625; DNAJPROTEIN.
SWART; SW00271; DNaJ; 1.
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PROSITE; PS50076; DNAJ 2; 1.
Chaperone; DNA replication; I
SEQUENCE 391 AA; 40914 MM
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SECUENCE FROM N.A.

MEDLINES-20450683; PubMed=10997877;

MEDLINES-20450683; PubMed=10997877;

Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;

"Prediction of the coding sequences of unidentified human genes.

"YVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

DNA Res 7:273-281(2000).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
30.0%; Score 58.5; DB 2; Length 678;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                Chissoe S., Hawkins J.;
"The sequence of C. elegans cosmid F52H2.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                    WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026214; AAB71311.1; -.
                                                                                                                                               Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                   Wilson R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                         PIR; T32483; T32483.
Wormbase; WBGene00018714; F52H2.1.
Wormbep; F52H2.1a; CE10864.
Hypothetical protein.
SEQUENCE 678 AA; 78262 MW; 49ABB6583D5919B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003961; FN III.
InterPro; IPR07110; Ig-like.
InterPro; IPR003598; Ig-c2.
InterPro; IPR01009; Kinase like.
InterPro; IPR00719; Prot Kinase.
InterPro; IPR008266; Tyr pkinase-AS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000001; Prot_kinase; 2
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PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIAA1639 protein (Fragment).
Name=KIAA1639;
Homo sapiens (Human).
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00069; Pkinase; 1
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SMART; SM00408; IGc2;
                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                            SEQUENCE FROM N.A. STRAIN=Bristol N2;
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    STRAIN=Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                       Waterston R.;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 15, Last annotation update)
01-OCT-2003 (TrEMBLrel. 12, Last annotation update)
Name=F52H2.1; ORFNames=F52H2.1,
Caenorhabditis elegans
Elwaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN:S2 / LL;
Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,
Conway de Macario E., Dodsworth J., Gillett W., Graham D.B.,
Modock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G.,
Saenphimmachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
Leigh J.A.;
Complete genome sequence of the mesophilic hydrogenotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2,
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WormBase Consortium;
"Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
                Query Match 30.8%; Score 60; DB 2; Length 391; Best Local Similarity 40.5%; Pred. No. 67; Matches 15; Conservative 6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 380;
86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methanogen Methanococcus maripaludis.";
submitted (PRB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BX95-222; CAF30796.1;
InterPro; IPR008829; SLA_LP_auto_ag.
Pffam; PF05889; SLA_LP_auto_ag; 1.
Complete proteome.
SEQUENCE 380 AA; 43377 WW; 22776AD3A010659F CRC64;
                                                                                                                                                                                                                                                                                                                                                                         Methanococcus maripaludis.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanococcaceae; Methanococcus.
                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 NLEREMINLAPIQRGGILPTESKKIIYE--YWDGYSVC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NKALELKNEQTLRADEILPSESKOKDYEESSWDSESLC 38
                                                                                                1 NKALELKONEQTLRADEILPSESKOKDYEESSWDSESL 37
                                                                                                                     678 AA.
                                                                                                                                                                                                                                        380 AA
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                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 39.54
Matches 15; Conservative
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Q6LXV6
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative DNA-binding protein.

ORFNames=OSJNBa0019M20.3;
Orgas astiva (japonica cultivar-group).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Enrhartoideae, Oryzeae, Oryza.
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Pred. No. 1.7e+02;
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                                                                                1319 AA; 142048 MW; FBA43AE17204EF48 CRC64;
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1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                   30.0%; Score 58.5; DB 2;
44.8%; Pred. No. 3.8e+02;
tive 8; Mismatches 7;
PS50011; PROTEIN KINASE DOM; 2.
PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence and analysis of rice chromosome 4.";
Nature 420:316-320(2002).
EMBL; AL606690; CAE03543.2; -.
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SEQUENCE FROM N.A.
The Rice Chromosome 10 Sequencing Consortium;
                                                                                                                                                                                                                                                                                      548 AA
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Name=OSJNBa0060D06.9;
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Best Local Similarity
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SEQUENCE 548 AA
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Q7XE90
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Q7XPN5
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Gaps
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"In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1066;
                                                                                                                            Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q., Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017097; AAP53900.1; -
                                                                                                                                                                                                              Gramene, Q7XE90; -...
GO; GO:0000151; C:ubiquitin ligase complex; IEA.
GO; GO:0003677; F:ubiquitin ligase activity; IEA.
GO; GO:0004647; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006270; F:zinc ion binding; IEA.
GO; GO:0016567; F:protein ubiquitination; IEA.
Interpro; IRR001841; Znf_ring.
SWART; SM00184; RING; 1.
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35.3%; Pred. No. 3.5e+02;
tive 8; Mismatches 14;
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                                                  Science 300:1566-1569(2003)
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hes 12; Conservative
                                                                                                        SEQUENCE FROM N.A.
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Search completed: August 1, 2005, 22:22:22 Job time : 14.6256 secs

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Abv22662 Human pro
Abv4323 Human pro
Aal10911 Human bro
Acr18085 Human pro
Acr81108 Breast ca
Abv43067 Human pro
Abv43206 Human pro
Abv41632 Human pro
Abv41632 Human pro
Abv41632 Human pro
Adv41632 Human pro
Adv41631 Human pro
Adv41631 Human pro
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Adv41691 Human pro
Adv41691 Human pro
Adv41691 Human pro
Adv42981 Human pro
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Aaf22972 Human pro

Aaf2291 Human pro

Aaf22991 Human pro

Aaf22986 Human pro

Aaf22986 Human pro

Aaf22989 Human pro

Aaf22989 Human pro

Aaf22967 Human pro

Aaf22969 Human bre

Aaf7722 Branan cDN
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Ad193129 Human bre
Ade44419 Human cDN
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Abv28376 Human pro
Abv27350 Human pro
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Human p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate expression marker cDNA 4081.
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ABV22558
ABV28376
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ABV34206
ABV34206
ABV341632
ADO40108
ACN92774
ACN97508
AAF22980
AAF22974
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AAF22286
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ABV13085
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16-MAR-2000; 2000US-0189662P.
25-MAY-2000; 2000US-0201454P.
9-UJN-2000; 2000US-0211014P.
18-UJL-2000; 2000US-021907P.
13-DEC-2000; 2000US-025281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV04090 standard; cDNA; 403
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  ABV04090;
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   -MODEL-frame+ p2n.model -DEV-xlp
-MODEL-frame+ p2n.model -DEV-xlp
-MODEL-frame+ p2n.model -DEV-xlp
-Qe/cgn2_1/USFYFO spool p/USO8489099/runat_01082005_141249_13290/app_query.fasta_1.1635
-DE-N Geneseq_16Dec04 -OFMT=fastap -SUFFIX=rng -MIRWATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cdi
-LIGT=45 -DOCALIGN=200 -THR SCORE-pcr -THR MATA=100 -THR MINE -0 ALIGGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAFSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=USO9489079_@CGN_1 _11418 @runat_01082005_141249_13290 -NCFU=6 -ICFU=3
-NO_MMAP -LARREQUERY -NGG_SCORES=0 -MATT -DSPBICCK=100 -LONGING
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Abv13259 Human pro
Acn90082 Breast ca
Abt22264 Breast ca
Aal18710 Human bre
                                                                                     August 1, 2005, 22:23:28 ; Search time 87.0391 Seconds (without alignments) 3196.585 Million cell updates/sec
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                GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                          of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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ABV13259
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AAL18710
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Fgapop 6.0 , Fgapext
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246
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (l) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAlaLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 404 BP; 138 A; 79 C; 100 G; 87 T; 0 U; 0 Other;
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                                                                                                                                                                        Claim 1; Page 2195; 11750pp; English.
                Monahan JE;
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                Endege WO,
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                                                   WPI; 2001-662795/76.
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                Schlegel R,
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                                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cell carcinogenic potential of a compound; (g) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 403 BP; 138 A; 79 C; 98 G; 87 T; 0 U; 1 Other;
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                Monahan JE;
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25-MAY-2000; 2000US-0207454P.
09-UUN-2000; 2000US-0211314P.
18-UUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
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                Schlegel R,
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Disclosure; Page 271; 725pp; English.

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The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that blinds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for invention may be described as cytostatic. The antibody is useful for a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 AAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; vaccine; breast cancer marker gene; breast mass; immunogen; chemotherapy; tumour burden; bait protein; two-hybrid; three-hybrid; surrogate marker gene; pharmacodynamic marker gene; transgenic animal;
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detecting presence of polypeptide in sample, as a marker for breast
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                                                Disclosure; SEQ ID NO 11232; 36pp; English.
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Best Local Similarity:
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The invention relates to an isolated polypeptide encoded by a breast cancer marker gene comprising any of 1417 21-805 nucleotide sequences, given in the specification. The methods of the invention are useful for diagnosing patients having an identified breast mass or symptoms associated with breast cancer, to diagnose breast cancer or its precursors, and for monitoring the efficacy of treatment of a breast cancer patient (e.g. efficacy of chemotherapy). The methods are also useful for evaluating a patient before, after or during therapy, to cretain are useful as patient before, ration antibodies, by immunishing a marmal with a breast cancer marker proteins are useful as bat proteins of two-hybrid assay, to identify other proteins which bind to or interact with the marker proteins. The breast cancer marker genes are useful as bat proteins which bind to or interact with the marker concern arker genes are useful as paticular, breast cancers. The breast cancer marker genes are useful as pharmacodynamic marker genes. An antibody which is electively binds to a protein of a breast cancer marker genes are useful to a protein of a breast cancer marker genes are useful for producing non-human transgenic animals. This invention is useful for producing non-human transgenic animals. This
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2000US-0192099P.
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2000US-0220534P
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29-MAR-2000;
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14-MAR-2000;
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25-JUL-2000;
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                                                                                                                                                                                                                                                                               Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                 The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is affilicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast calls. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, markersing treating and polypeptides are polynucleotides and encoded polypeptides. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                  New peptide useful as a marker for the diagnosis of breast cancer
                                                                                                                                                                          Sequence 434 BP; 141 A; 81 C; 92 G; 120 T; 0 U; 0 Other;
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                 GluLeuMetAspMetGlnThrPheLysAla 30
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                 Steinmann K;
                                                                                                                                                                                                                                                              US-09-489-079-28 (1-47) x AAL18710 (1-434)
                                                                    Claim 1; Page 1991; 3695pp; English.
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25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
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                 Wang Y,
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                                  WPI; 2001-451856/48
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Best Local Similarity:
                 Χn Y,
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                 Lillie J,
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (d) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                            Page 5949; 11750pp; English.
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2000US-0189862P.
2000US-0207454P.
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2000US-0219007P.
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18-JUL-2000;
13-DEC-2000;
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25-MAY-2000;
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WPI; 2001-662795/76
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                                                                                                                                        The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call cardinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (i) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 444 BP; 144 A; 91 C; 115 G; 94 T; 0 U; 0 Other;
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Mismatches:
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                                                                                                     Claim 1; Page 7224; 11750pp; English.
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2000US-0189862P.
2000US-0207454P.
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit in prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer mas metastasized in a patient; (f) assessing the prostate cancer has metastasized in a patient; (g) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                         Claim 1; Page 3975; 11750pp; English.
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16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
9-UJN-2000; 2000US-0211314P.
18-UJJ-2000; 2000US-021907P.
13-DEC-2000; 2000US-025281P.
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibit ing prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) assessing the prostate cancer in a patient; (f) assessing the prostate cancer in a patient; (f) assessing the prostate cancer in a patient; (d) assessing the prostate cancer in a patient; (d) assessing the prostate cancer has metastisated in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAlaLeu
                                                                                                                                                                                                                                                                                                           Sequence 444 BP; 144 A; 91 C; 115 G; 94 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluLeuMetAspMetGlnThrPheLysAla 30
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                                                                         Claim 1; Page 8627; 11750pp; English.
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25-JUL-2000; 2000US-0220534P.
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Best Local Similarity:
Query Match:
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14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
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Pred. No.:
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349 AAGGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                    1 LysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAlaLeu
            peptide useful as a marker for the diagnosis of breast cancer.
                                                                                                                                                                                                                        Sequence 454 BP; 125 A; 91 C; 89 G; 148 T; 0 U; 1 Other;
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                                         Claim 1; Page 620; 3695pp; English.
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Query Match:
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                 The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (d) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                               The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds
                                                                                                                                                                 Sequence 466 BP; 171 A; 87 C; 104 G; 104 T; 0 U; 0 Other;
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 Claim 1; Page 2161; 11750pp; English.
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Best Local Similarity:
Query Match:
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invention may be described as cytostatic. The antibody is useful for detecting the presence of (1) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (1) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 AAGGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSexIleProThrLysAlaLeu
                                                                                                                                                                                                                                                                     Sequence 470 BP; 127 A; 97 C; 93 G; 149 T; 0 U; 4 Other;
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Matches:
Conservative:
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16-MAR-2000; 2000US-0189662P.
25-MAY-2000; 2000US-0207454P.
9-UJN-2000; 2000US-0211314P.
18-UJL-2000; 2000US-021907P.
13-DEC-2000; 2000US-021907P.
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progression of prostate cancer in a patient; (c)
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progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 AAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAGTTTCTATTCCAACTAAAGCCTTA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAlaLeu
                                                                                                                                                                                                Sequence 473 BP; 162 A; 91 C; 115 G; 105 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate expression marker cDNA 34197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATIGATGGACATGCAAACTTTCAAAGCA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluLeuMetAspMetGlnThrPheLysAla 30
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                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                             (1-473)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР
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2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
                                                                                                                                                                                                                                                                                                                                                                                                             x ABV43067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0255281P
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100.00$
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                                                                                                                                                                                                                                                                                                                                                                                                             US-09-489-079-28 (1-47)
                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
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Pred. No.:
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ABV34206
                                                                                                                                                                                                                                                                                    Score:
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the
of a test compound to inhibit prostate cancer in a patient, (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient
                                                                                                                                                                                                                                                                                                                      Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                   ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                               Sequence 473 BP; 162 A; 91 C; 115 G; 105 T; 0 U; 0 Other;
                                                                                                                                                                              473
30
0
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                               Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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, 2000US-0189862P.
, 2000US-0207454P.
, 2000US-0211314P.
, 2000US-0219007P.
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25-MAY-2000;
09-JUN-2000;
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                                                                                                                                                                Alignment Scores:
Pred. No.:
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us-09-489-079-28.rng

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progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasaized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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Aliqnment Scores:			
Pred. No.:	4.41e-15	Length:	508
Score:	152.00	Matches:	30
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Ouery Match:	61.79%	Indels:	0
DB:	2	Gaps:	0

Sequence 508 BP; 176 A; 100 C; 120 G; 111 T; 0 U; 1 Other;

US-09-489-079-28 (1-47) x ABV03916 (1-508)

265 AAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGGCCTTA 324 1 LysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAlaLeu 20 셤 ઠે

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Search completed: August 1, 2005, 23:18:16 Job time: 91.0391 secs

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000 0111111111111111111111111111111111		RESULT 1 AL357148 LOGENTION DEFINITION ACCESSION VERSION VERYWORDS SOUNCE ONGANISM AUTHORS TITLE JOURNAL COMMENT
GenCore versi Copyright (c) 1993 - 200 in - nucleic search, using frame_L August 1, 2005, 22:24:58 US-09-489-079-28 score: 246 : KDGLLKANCGMKVSIPTKAL table: BLOSUMG: Kgapop 10.0, Kgapext 0.5 Kgapop 10.0, Kgapext 0.5 Fgapop 6.0, Fgapext 7.0 Fgapop 6.0, Fgapext 7.0		Database: General: * 1:

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Direct Submission
Submitted (01-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. B-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 2, 2003 this sequence version replaced gi:11139963.
                                                                                                                                                                                                                                                                                                                            Assembly program: XGA64; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemietry: Dye-terminator Big Dye; 100% of reads Consensus quality: 180973 bases at least Q40 Consensus quality: 182878 bases at least Q30 Consensus quality: 183958 bases at least Q30 Insert size: 341919; sum-of-contigs Quality coverage: 2.72x in Q20 bases; sum-of-contigs Quality coverage: 2.72x in Q20 bases; sum-of-contigs Quality coverage: 5.31x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 11652 bp in length 1: gap of 100 bp in length 1: gap of 100 bp in contig of 8319 bp in length 1: gap of 100 bp in contig of 100 bp in length 2: gap of 100 bp in length 3: gap of 100 bp in length 3: gap of 100 bp in length 2: contig of 135726 bp in length 2: contig of 135726 bp in length 2: gap of 100 bp in length 3: contig of 20726 bp in length 3: contig of 20726 bp in length 3: contig of 30554 bp in length.
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/note="assembly fragment:01291
fragment_chain:1"
20172. :50720
/note="assembly_fragment:01448
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/note="assembly_fragment:00451
                                                                                                                                                                                                                                      Contact: humquery@sanger.ac.uk
                                                                                                                                                                                         Center code: SC
Web site: http://www.Banger.ac.uk
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/organism="Homo sapiens'
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                       Center project name: bB263N18
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                                                                                                                      COMMENT
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on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence characted from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 RP11-739D18 is from the library RPCI-11.3 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 GlyMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLys 29
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 343019)
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Homo sapiens chromosome 10 clone RP13-263N18, *** SEQUENCING IN
PROGRESS ***, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36371 GCAGGTAAATTTTGTAATTTTTAATTTTTACTCTGGAAAGAAGAAGAATTTTAAAATTTTACTTTACTCTGGAAAGAAGAAAAATTTTAAATAT 36424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                             --- Genome Center
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AP006565 93824 bp DNA linear PRI 13-AUG-2003 Homo sapiens genomic DNA, chromosome 18 clone:RP11-1157N02_B, complete sequence.
AP006565 AP006280
AP006565.1 GI:33620418
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2 (bases 1 to 37716)
Hattori,M., 18hii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Sada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Bliect Submission
Submitted (25-JUN-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Aug 11, 2003 this sequence version replaced gi:32306455.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Published only in Database (2003)
2 (bages 1 to 93824)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
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Matches:
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Nordaiek, G., Conrad, A., Dose, S., Grimm, M., Groet, J., Hornischer, K., Loehnert, T.H., Nizetic, D., Scharfe, M., Schoen, O., Yaspo, M.L. and
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On Dec 3, 1999 this sequence version replaced gi:4894179.
Collaborators:
Collabo
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Ihnestrasse 73, D-14195 Berlin-Dahlem, Germany
All annotations in this database entry are developed by
computational tools. It is therefore not explicitly noted in the
feature lines that evidence is not experimental.
PROGRAMS AND PARAMETERS USED FOR ANNOTATION:
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Homo sapiens chromosome 21 BAC RGB62L20, complete sequence.
AL050302
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Mascheroder Weg 1, D-38124 Braunschweig, Germany
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Matches:
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Mismatches:
Indels:
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3loecker, H.
                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                    Alignment Scores:
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ACCESSION
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KEYWORDS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
HSB62L20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
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Minimum score: 60; Minimum identity: 90 %;

Yandem Repeats': GDE 2.2 option 'tandem'

Yandem Repeats': GDE 2.2 option 'tandem'

Yandem Repeats': GDE 2.2 option 'pp;

Inverted Repeats': GDE 2.2 option 'inverted'

Yinco Satellites': GDE 2.2 option 'sputnik' (Abajian) > 'CpG

Islands': GDE 2.2 option 'cpg'

CpG island region size 100 bp;

Margin: 50; Number of mismatches allowed: 0; Word size: 7 .

STS database: 'dbSTS markers'

YENN Scan': tRNAScan-SE (Lowe & Eddy), Vers: 1.11 Sequence

overlaps with Acc.Nrs. Aloges and ALO78475.
                                                                                                                                                                                              . Prior probability: 0.04; Overlapping number: 0 > Xpound (Thomas & Skolnick)
                                                                                                                                                                                                                                                       Base score cutoff: 0.2; Minimal exon length: 3 bp > 'Repeats':
BLASTN 2.0.9 (Altschul et al.)
Database(s): * RepBase (human), released 22-DEC-1995 .

* RepBase (mammal), released 22-DEC-1995 .

Minimum identity: 70 %;
> 'EST9: BLASTN 2.0.9 (Altschul et al.)
Database(s): * embl (EST), Vers. 60 (16-SEP-1999) .

Using sequence with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Using sequence with
                           /clone="RGB62L20"
complement((1.14). .(75.155))
/note="match: ESTs AA825445 A1018653 A1792286 A1792327"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="86% identity: matches 176. .272 of consensus"
/rpt_family="AluSg"
complement(618. .682)
/rpt=family="Li"
/rpt_family="Li"
686. .729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: EST AW001671"
complement (436. .565)
/note="83% identity: matches 463. .592 of consensus"
/rpt_family="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43. -564 'note="86% identity: matches 12. .133 of consensus" rrpt_family="AluSz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="IR1, 79% complementary to IR1' (931. .1069)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Programs used by 'AnnoMitter':
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="homology = 79.5%, counts = 11"
/rpt_family="aata repeat"
/rpt_type=TANDEM
689. 708
                                                                        Organism: human
> GenScan (Burge & Karlin), Vers. 1.0
Used matrix: vertebrate; Minimum score: 0
> Grail (Xu et al.), Vers. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .119182
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
                                               > GeneFinder (Green), Vers. 084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_type=INVERTED
578...677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   map="21q11.1"
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exon	;	/note="match: GSSs AG020
	/HOCE="GENSIAN PICTURE, SCORE = 0.00 GRAIL, SCORE COMMENT = excellent MYRP nrediction 100%, comment = 0.000	repear_region 0050: .v.co /note="IR2, 84% complet /rot type=INVERTED
repeat_region	7.75	repeat_region 60396283 /notea=#87% identity: m/ /rot family=#131.5G"
repeat_region	7.15 1980 970 1980 Angelengy identity: matches 175286 of consensus"	repeat_region complement (60456170) //note=*90% identity: mat/rrt familv="11" in the family in th
repeat_region	Complement (9731080) Complement (9731080) /note="88% identity: matches 157265 of consensus" /rot family="AluSq"	misc_feature
repeat_region	complement(1124. 1209) /note="89" identity: matches 37122 of consensus" /not family-maluscy:	
exon	1407 - 1407 - 1407 - 1407 - 1407 - 1407 - 1407 - 1407 - 1407 - 1601 - 16	exon 66616729 /note="XPOIND prediction
exon	1479. 1507. 1479. 1507. The description acres - 0.572"	Alignment Scores:
misc_feature	/moce="match: GSSB AG014201 AG014202 AG014200"	4.14e-14
misc_feature	complement((1885.2240)(1922.2547)) /note="match: GSSB AG014203 AG014204 AG014207 AG014206 AG014304	Percent Similarity: 51.28% Consex Best Local Similarity: 46.15% Mismat Onery March: 70.12% Indels
repeat_region	25482593 /note="homology = 95.7%, counts = 23"	6
	/rpt_ramily="ac_repeat" /rpt_type=TANDEM	T) 02020201 ((\$-T)
satellite	25482582 /note="AC repeat"	
misc_feature	(2595.3250)(2828.3328) /note="match: GSSs AG014196 AG014199 AG014198 AG014200	Db 70066 AAGATGGTCTTCTGAAGGTAATAACTTTTT
misc_feature	AG01419/' complement ((2595.3149)(2839.3328)) /nore="march: GSSR AG014210 AG014209 AG014208 AG014207"	Db 70126 TTTATGAAGTATACATTATATAGTAATTAT
repeat_region	of conge	Ov 10 GlvMetLvsValSerIleProThrLvsAlal
toorer teener		70186
	Compression (2017) (201	90
misc_feature	/ LPC LAUMLIY="LL" (3636_3811). (3916.4117) /note="match: GSSs AG014196 AG014195 AG014194"	702
misc_feature	complement (3636 . (3802.4038)) /nore=ment(3636 . (3802.4038))	RESULT 6
exon	/morplement (4600 . 4610) /more="XXXVIIII Drediction: score = 0.222"	AP005213 LOCUS AP005213 162364 bp
repeat_region	8 identity: matches 12	z
repeat_region	y="AluSq" (47805040)	z
I	/note="85% identity: matches 164424 of consensus" /rpt family="11"	KEYWORDS HTG. SOURCE Homo sapiens (human)
	%0.0te="XPOUND prediction, score = 0.495"	
	/note="XPOWIN prediction, score = 0.201"	REFERENCE 11 TONIA W TONIA W
misc_teature	complement(51605197) /note="match: BSTs AW128901 AW128885"	
eature	complement(51645201) /note="match: GSS AQ883466"	
repeat_region	5251 .5286 /note=nhomology = 97.2%, counts = 18"	REFERENCE 2 (Dases 1 to 162364) AUTHORS Hattori,M., Ishii,K., Toyoda,A.,
gatellite	/rpt_type=TANDEM /rpt_type=TANDEM 5255286	TITLE Direct Submission JOURNAL Submitted (17-MAY-2002) Massahira
ture	/note="TG repeat" complement (5355.5370)(5388.5427)) /note="march: Fera broads brackork bw024170"	and Chemical Research (RIKEN), Ge 1-7-22 Suehiro-chou, Tsurumi-ku,) (E-mail:hattori@esc.riken.go.ip,
exon	55855646 /note="XPOUND prediction, score = 0.256"	Tel:81-45-503-9111, Fax:81-45-503 COMMENT On Jul 10, 2002 this sequence ver
misc_feature		FEATURES Location/Qualifiers

aleugluleuwetaspwetginthrphelys 29 TTGTGTTTTCCAAACCCATTTAGCCTACCTGT 70185 TATATTTTTATCTTGAATATTAACTACTTAT 70125 ra Hattori, The Institute of Physical Genomic Sciences Center (GSC); Y Yokohama, Kanagawa 230-0045, Japan p, WEL:http://hgp.gsc.riken.go.jp/, 503-9170) version replaced gi:21327928. DNA linear PRI 11-JUL-2002 osome 18 clone:RP11-97024, complete raniata; Vertebrata; Euteleostomi; atarrhini; Hominidae; Homo. σ . . (6669.7116)) 13829 AG013831 AG013833 AG013830" -----AsnCys rLeuGluargArgIleLeuLysTyr 47 |:::||| ||| |||||||| rGrGGAATTAAGAACATTAAAATAT 70299 mentary to IR2' (7549. .7799)" atches 301. .424 of consensus" atches 9. .255 of consensus" , Taylor, T.D., Hong-Seog, P., ., Taylor, T.D., Hong-Seog, P., , Watanabe, H. and Sakaki, Y. 56%, comment = good" on, score = 0.372" 119182 36 4 7 31 13851 AG013852" 20269 AQ883588" gth: ches: servative: matches: els:

9

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consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                               26049: contig of 26049 bp in length 26149: gap of 100 bp 29660: contrig of 3511 bp in length 29760: gap of 100 bp 37939: contrig of 8179 bp in length 37939: contrig of 8179 bp in length 42120: contrig of 4081 bp in length 42220: gap of 100 bp 44683: contrig of 2463 bp in length 44783: gap of 100 bp 47964: contrig of 2181 bp in length 47964: contrig of 7181 bp in length 48664: gap of 100 bp 55658: contrig of 74123 bp in length 55758: gap of 100 bp 129881: contrig of 74123 bp in length 129881: contrig of 74123 bp in length 134693: contrig of 4712 bp in length 134693: contrig of 58897 bp in length 134793: gap of 100 bp
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36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol type="genomic DNA"
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1. 26049
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Matches:
Conservative:
Mismatches:
Indels:
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134794. .190690
/note="assembly_fragment:04764"
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/organism="Homo sapiens"
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51.28%
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Best Local Similarity:
Query Match:
DB:
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38040
42121
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48065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131696 TTTATGAAGTATACATTATATAGTAATTATTGTGTTTCCAAACCCATTTAGCCTACCTGT 131755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL627234 190690 bp DNA linear HTG 31-OCT-2001
Homo sapiens chromosome 13 clone RP11-53904, WORKING DRAFT
SEQUENCE, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 GlyMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLys 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Buteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LysAspGlyLeuLeuLysAla------
                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AsnCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Sequencing vector: plasmid; L08752; 100% of reads
Consensus quality: 187938 bases at least Q40
Consensus quality: 188704 bases at least Q20
Insert size: 198790; sum-of-contigs
Insert size: 198444; 3.4% error; agarose-fp
Coulity coverage: 10.55x in Q20 bases; sum-of-contigs Quality
coverage: 10.32x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL627234.8 GI:16596759
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
HOMO sapiens (human)
                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: bA53904
 1. .162364
/organiem="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
/chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-162364)
                                                                                                                                                                                                                                                                                Gaps:
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Primates;
                                                                                          /map="18p"
/clone="RP11-97024"
                                                                                                                                                                                                                                                                                                                     US-09-489-079-28 (1-47) x AP005213
                                                                                                                                                                           5.74e-14
172.50
51.28%
46.15%
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Mammalia; Eutheria;
                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                      Alignment Scores:
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DB:
   source
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KEYWORDS
SOURCE
ORGANISM
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AL627234/c
                                                                                                                                                                                         . No. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
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map="21q11.1"
/clone="P127M18, 5' partial"
/clone lib="RPC11,3-5 PAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="Pi6C2, 5' partial"
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59858. .179140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="RPCI1,3-5 PAC library"
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237516. .>340000
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104370. .179507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="R663H15, 3' partial"
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    e.mail: info-chr2l@molgen.mpg.de
    URL: http://chr2l.rz-berlin.mpg.de/.
Location/Qualifiers

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/rpt_type=DISPERSED
2530_.2654
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 34000)

S Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Troydda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E., Polley,A., Menzel,U., Delbar,J., Kumpf,K., Lehmann,R., Polley,A., Menzel,U., Delbar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schlubya,K., Kawasaki,K., Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S., Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G., Hornischer,K., Brandt,P., Schoen,O., Desario,A., Klages,S., Hennig,S., Riessellmann,L., Dagand,E., Wehrmeyer,S., Borzym,K., Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
                                                                                                                                                                                                                                                                                           33516 TITATGAAGTATACATTATATAGTAATTATTGTGTTTCCAAACCCATTTAGCCTACCTGT 33457
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The Chromosome 21 Mapping and Sequencing Consortium consists of * RIKEN Genomic Sciences Center, Human Genome Research Group, *
                                                                                                                                                                                                                                                           10 GlyMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLys 29
                                                                                                                                                           ----AsnCys 9
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* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
info.genome@gbf.de
                                                                                                                                                                                                                                                                                                                                                              30 AlaglytysPheCysAsnPheAsnPheThrLeuGluArgArglleLeuLysTyr 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * Institute of Molecular Biotechnology, Genome Analysis, * Beutenbergstrasse 11, D-07745 Jena, Germany, * e.mail: gscj-submit@genome.imb-jena.de * URL: http://genome.imb-jena.de/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340000 bp DNA 11
Homo sapiens chromosome 21 segment HS21C003.
AL163203 AP001658 BA000005
AL163203.2 GI:7717244
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• e.mail: shimizu@dmb-med.keio.ac.jp
• URL: http://adenine.dmb.med.keio.ac.jp/
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* e.mail: sakaki@gsc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
        US-09-489-079-28 (1-47) x AL627234 (1-190690)
                                                             LysAspGlyLeuLeuLysAla-----
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SOURCE
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COMMENT

us-09-489-079-28.rge

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109016 AAAGATGGTCTTCTGAAGGTAATAACTTTTTATATTTTTATCTTGAATATTAACTACTTAT 108957 108956 TTTATGAAGTATACATTATATAGTAATTATTGTGTTTCCAAACCCATTTAGCCTACCIGT 108897 Length:
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Conservative:
Mismatches:
Indels: 1 LysAspGlyLeuLeuLysAla------US-09-489-079-28 (1-47) x HS21C003 (1-340000) Gaps: /rpt_type=Dispersed 1.25e-13 172.50 51.28% 46.15% 8 -----Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.:

Query Match: DB:

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10 GlyMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLys 29 RESULT 9 AP003901/c LOCUS DEFINITION ò 셤 ઠે 셤

73775 bp DNA linear PRI 15-MAR-2003 complete sequences. Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo AP003901.1 GI:14646859 Homo sapiens (human) Homo sapiens VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS ACCESSION

Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Hong sapiens genomic DNA Hong sapiens genomic DNA LD Stated Only in Database (2001)

2. (Dases I to 73775)

B. Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission

L. Submitted (05-JUL-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemilihattoriogesc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

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Conservative:
Mismatches:
Indels:
Gaps: 1.21e-13 168.00 87.18% 76.92% 68.29% Percent Similarity: Best Local Similarity: Query Match: DB: Pred. No.: Score:

US-09-489-079-28 (1-47) x AP003901 (1-73775)

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                              Schlegel, R., Endege, W.O. and Monahan, J.E.
Genes differentially expressed in human prostate cancer and their
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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Seguence 13250 from Patent WO0160860.
CQ481383
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B. 2 (bases 1 to 127500)

E. 2 (bases 1 to 127500)

E. 3 (bases 1 to 127500)

E. 4 Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission

E. Submitted (08-MUG-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suchiro-chou, Tsurumi, Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-85-503-9111, Fax:81-45-503-9170)

On Aug 12, 2003 this sequence version replaced gi:32400665.
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Homo sapiens genomic DNA, chromosome 18 clone:RP11-1157N02_A,
complete sequence.
                  PAT 30-JAN-2004
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                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                LysklaglyLysPheCysksnPheAsnPheThrLeuGluArgArglleLeuLysTyr 47
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Sequence 4081 from Patent WO0160860.
CQ472214 GI:41437833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="18"
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/clone="RP11-1157N02_A"
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166.00
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PAT 30-JAN-2004

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CQ496633
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                                                        PAT 28-JAN-2004
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genes differentially expressed in human prostate cancer and their
                                                                                                                                                                                           Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of breast cancer
Patent: WO 0151628-A 11177 19-JUL-2001,
Millennium Pharmaceuticals, Inc. (US)
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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                                                     CQ426143 434 bp DNA Sequence 11177 from Patent W00151628. CQ426143 GI:41378372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378 GAATTGATGGACATGCAAACTTTCAAAGCA 407
  233 GAATTGATGGACATGCAAACTTTCAAAGCA 262

    .434
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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CQ490788
                             RESULT 13
CQ426143
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PAT 30-JAN-2004
                                 213 AAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 272
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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                                                                                                     273 GAATTGATGGACATGCAAACTTTCAAAGCA 302

    .444
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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US-09-489-079-28 (1-47) x CQ490788 (1-444)
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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August 1, 2005, 22:08:06; Search time 2.89573 Seconds (without alignments) 1561.672 Million cell updates/sec Run on:

US-09-489-079-28 246 1 KDGLLKANCGMKVSIPTKAL.....FKAGKFCNFNFTLERRILKY 47 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	hypothetical prote	ᆽ	interleukin-1 beta	>-	SNF2 helicase BH09	hypothetical prote	atp-specific succi	extragenic suppres	conserved hypothet	xanthosine phospho	probable two-compo	hypothetical prote	farnesyl-pyrophosp	glutamate ionotrop	glutamate receptor	probable chloroqui	probable chloroqui	giant protein p619	extragenic suppres	probable membrane	DNA-directed RNA p	hypothetical prote	intercellular adhe	cadmium-transporti	probable periplasm	heat shock protein	glutamate synthase	leucine-tRNA ligas	hypothetical prote
QI 1	B97228	T13889	JC5646	B72409	A83771	E97701	T41038	AB1208	F82983	: AI0143	: E96020	: T05759	: T03687	: JH0826	. JS0685				: AE1564	: B81376	: F75461	: T34140	: JC5018	: D84154	: E81328	. A41252	: E69006	₹"	T24683
Length DB	461 2	1441 2	214 2	404	577 2	175 2	433 2	257 2	529 2	287 2	225 2	278 2	353 2	926	926		2819 2		257	538	1546	248	544	707	846	405	622	792	1872 2
& Query Match	26.2	26.0	22.6	22.6	22.4	22.0	22.0	21.5	21.5	21.3	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.1	20.7	20.7	20.7	20.5	20.5	20.5	20.5	20.3	20.3	20.3	20.3
Score	64.5	64	55.5	55.5	22	54	54	53	53	52.5	52	52	52	52	25	52	52	52	51	51	51	50.5	50.5	50.5	50.5	20	20	20	20
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hypothetical prote	probable membrane-	hypothetical prote	hypothetical prote	biotin carboxylase	hypothetical prote	S2 ribosomal prote	ribosomal protein	sugar permease hom	glyceraldehyde-3-p	pyruvate formate-1	hypothetical prote	hypothetical prote	hypothetical prote	genome polyprotein	epidermal growth f
\$69804	D95925	T21766	D64373	A70432	T05335	E86577	H72044	E70018	DELOG3	A69416	B81287	T05578	C84547	RRNZA2	B45558
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49.5	49.5	49.5	49.5	49.5	49.5	49	49	49	49	49	49	49	4	49	48.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A;Residues: 1-461 «KUR»
A;Cross-references: UNIPROT:Q97FR1; GB:AE001437; PIDN:AAK80613.1; PID:g15025696; GSPDB:
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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T13889
helicase II homolog - fruit fly (Drosophila sp.)
C;Species: Drosophila sp.
C;Species: Drosophila sp.
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13889
R;Gillespie, D.E.; Bergy C.A.
Genes Dev. 9, 2495-2508, 1995
A;Title: Homeless is required for RNA localization in Drosophila oogenesis and encodes A;Accession: T13806; MUID:96033800; PMID:7590230
A;Reference number: Z17806; MUID:96033800; PMID:7590230
A;Reference number: Z17806; MUID:96033800; PMID:7590230
A;Reference number: A;Cross-references: UNIPROT:Q26453; EMBL:S79915; NID:g1195547; PIDN:AAB35476.2; PID:g73
A;Genetics:
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Matches 16; Conserv
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9KE87; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB046
A;Experimental source: strain C-125
A;Genetics:
A;Gene: BH0969
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A;Status: preliminary
A;Molecule type: DNA
A;Molecules: 1-175 <KUR>
A;Cross-references: UNIPROT:Q92JQ4; GB:AE006914; PIDN:AAL02551.1; PID:g15619046; GSPDB:G
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C.Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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A;Cross-references: UNIPROT:094415; EMBL:AL034491; PIDN:CAA22492.1; GSPDB:GN00068; SPDB:
A;Experimental source: strain 972h-; cosmid c1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypochetical protein RC0013 [imported] - Rickettsia conorii (strain Malish 7)
hypochetical protein RC0013 [imported] - Rickettsia conorii
C;Species Rickettsia conorii
C;Species 10-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 16-Aug-2004
C;Accession: E97701
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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C;Superfamily: succinate-CoA ligase (ADP-forming) beta chain
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C;Superfamily: ATPase involved in cell wall synthesis
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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7
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Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                           8; Mismatches
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109 KLITRQTGPAGKICNVVYVCERKFIR 134
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Pred. No.
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                                                                                                                                                                                                                                                                 22.4%;
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ilarity 33.3%;
Conservative 8
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38.5%;
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CiSpecies: Equas caballus (domestic horse)
CiSpecies: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
CiAccession: JC5646
R; Kato, H.; Youn, H.Y.; Ohashi, T.; Watari, T.; Goitsuka, R.; Tsujimoto, H.; Hasegawa, A Gene 177, 11-16, 1996
A; Title: Identification of an alternatively spliced transcript of equine interleukin-1 b A; Reference number: JC5646, MUID:97080493; PMID:8921838
A; Reference number: JC5646
A; Millo: JC5646
A; Reference number: JC5646
A; Residues: 1-214 «KAT>
A; Residues: 1-214 «KAT>
A; Residues: 1-214 «KAT>
A; Cross-references: UNIPROT: Q28386; DDBJ: D42165; NID: 92463549; PIDN: BAA22558 1; PID:9246
C; Comment: This protein mediates a variety of physiological response to infections and is synthesis by hepatocytes, and stimulation of chondrocytes and synovial cells to produce C; Superfamily: interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72409
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-404 cARN>
A;Experimental source: strain MSB8
A;Experimental source: strain MSB8
A;Experimental source: strain MSB8
A;Genetics:
C;Genetics:
C;Genetics:
C;Superfamily: S-adenosyl-L-homocysteine hydrolase, archaeal SAHH type
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SNF2 helicase BH0969 [imported] - Bacillus halodurans (strain C-125)
C;Species Bacillus halodurans
C;Species Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A83771
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Axids Res 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83569; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adenosylhomocysteinase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #text_change 09-Jul-2004
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: B72409
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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                                                                                                                                                                                                interleukin-1 beta - horse
C;Species: Equus caballus (domestic horse)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 22.6%; Score 55.5; DB 2; Length 214; Local Similarity 33.3%; Pred. No. 4.8; Nes 15; Conservative 7; Mismatches 16; Indels 7.
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                              ETGCGKTTOVPOYILD----EGYKSGKYCNIVVTOPRRI 173
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KANCGMKVSI PTKALELMDMQTFKAGKFCNFNFTLERRI
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Pred. No. 9.
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A;Accession: A10143
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-287 <KUR>
A;Cross-references: UNIPROT:Q8ZGV4; GB:ALS90842; PIDN:CAC90012.1; PID:g15979234; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Residues: -1725 - CAURA A, RESIDENCIA CACA9929.1; PID:G15141317; GSPDB:GResidues: -1725 - CAURA A, CTOSS-references: UNIPROT:Q92TSO; GB:AL591985; PIDN:CACA9929.1; PID:G15141317; GSPDB:GRESIDENCE: Strain 1021, megaplasmid pSymb R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, R; Galibert, F.; Finan, T.W.; Jones, T. Cowie, A.; Davis, R.W.; Joneso, S.; Federspiel, N.A.; Fisher, R.F. L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A, Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K, A; Pittle: The composite genome of the legume symbiont Sinorhizobium meliloti.
A, Reference number: A96039; MUID:21368234; PMID:11474104
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05759
R;Bevan, M.; Reichert, B.J.; Barel, E.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schue, aubmitted to the protein Sequence Database, June 1998
A;Reference number: 215450
A;Accession: T05759
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Mature 413, 523-577, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A;Genome: plasmid
C;Superfamily: ompR protein; response regulator homology
                                                                                                                                                                                                                                                                                                                                                                              5,
                                                                                                                                                                                                                                                                                  A,Gene: xapA
C,Superfamily: purine-nucleoside phosphorylase
C,Keywords: glycosyltransferase; pentosyltransferase
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Pred. No. 15;
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              Score 52.5; |
Pred. No. 17;
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SSAGMPIEIPARELGLLELLFMRAGK 167
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Local Similarity 34.6%;
Hes 9; Conservative
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Best Local Similarity 37.8%;
Matches 17; Conservative
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A,Accession: P82983
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-529 <STO>
A,Coss-references: UNIPROT:Q9HTP4; GB:AE004943; GB:AE004091; NID:g9951615; PIDN:AAG0869
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: A10143
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.J.; Br
K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Pseudomonas aeruginosa (strain PAO1)
                                                                                                              extragenic suppressor protein SuhB and to myo-inositol-1(or 4)-monophosphatase homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olaon, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Pseudomonas aeruginosa
Date: 15-8ep-2000 #sequence_revision 15-8ep-2000 #text_change 09-Jul-2004
                                                                                                                                       Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KALELMDMQTFKAGKFCNFN 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KDGLL----KANCGMKVSIPTKALELMDMQTFKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 13;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein PA5310 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 21.5%; Score 53; Best Local Similarity 40.0%; Pred. No. 3 Matches 14; Conservative 6; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: cardiolipin synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.5%;
Best Local Similarity 30.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KDGLLKANCGMKVSIPT
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Accession: F82983

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C, Genetics: A, Gene: PA5310 C, Superfamily:

AI0143

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216 IIHANASMSHTILLKAAELGMVSAYYTYIFTNLEFSLQR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 IIHANASMSHTILLKAAELGMVSAYYTYIFTNLEFSLQR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LLKANCGMKVSIPTKALELMDMQTFKAGKFCNFNFTLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LLKANCGMKVSIPTKALELMDMQTFKAGKFCNFNFTLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;591-609/Domain: transmembrane #status predicted F;620-638/Domain: transmembrane #status predicted F;805-825/Domain: transmembrane #status predicted
   transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: August 1, 2005, 22:23:22 Job time : 4.89573 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S18266
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                             21.1%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                        13; Conservative
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       F;549-566/Domain:
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                                                                                                                                                                                                                                                                                                             Query Match
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July 1826

Glutamate ionotropic receptor EAA1 chain precursor - human
NyAlternate names: Kahinate receptor chain
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Stepesion: July 1994
N;Tille: Molecular cloning, expression, and pharmacological characterization of humEAA1,
A;Reference number: JUN0826, MUID: 94087185; PMID: 8263508
A;Accession: JH0826
A;Molecule type: mRNA
A;Residues: 1-956 «KAMA
A;Residues: 1-956 «KAMA
A;Residues: 1-956 «KAMA
A;Coss: references: UNIPROT: Q16089; GB: S67803; NID: G544589; PIDN: AAB29311.1; PID: G544590
C;Comment: This protein mediates neurotoxicity of kainate
C;Comment: This protein mediates neurotoxicity of kainate
C;Superfamily: glutamate receptor; phosphoprotein; transmembrane prote
F;1-20/Domain: signal sequence #status predicted <SIG>F;21-956/Product: glutamate receptor hum EAA1 chain #status predicted <MAT>
F;420-838/Domain: glutamate receptor homology <GRH>
F;420-838/Domain: glutamate receptor homology of RH
F;420-838/Domain: glutamate receptor ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     furnesyl-pyrophosphate synthetase - rice
N;Contains: dimethylallyltranstransferase (EC 2.5.1.1); geranyltranstransferase (EC 2.5.
C;Specias: Orza sativa (rice)
C;Specias: Orza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03687
R;Sanniya, K.; Iwasaki, T.; Matsuoka, M.; Miyao, M.; Yamamoto, N.
B;Ochim. Biophys. Acta 1350, 240-246, 1997
A;Reference number: Z15009; MUID:97214636; PMID:9061016
A;Recession: T03687
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Restence number: 215009; MUID:97214636; PMID:9061016
A;Accession: T03687
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Restence unkpr: Assans
A;Restence unkpr: Assans
A;Restence unkpr: Toylogal and the blue-light
A;Restence and pyrophosphate forming farnesyl diphosphate with dimethylallyl
A;Restence and pyrophosphate synthetase
C;Reywords: isoprenoid biosynthesis; multifunctional enzyme; transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
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A,Molecule type: DNA
A,Residues: 1-278 <BEV>
A,Cross-references: UNIPROT:081838; EMBL:AL030978
A,Cross-references: UNIPROT:081838; EMBL:AL030978
A,Fxperimental source: cultivar Columbia; BAC clone M4122
C,Genetics:
A,Fxperimental source: altivar AA,Introns: 159/3
A,Introns: 159/3
A,Note: M4122.160
C;Superfamily: Arabidopsis thaliana hypothetical protein M4122.160
                                                                                                                                                                                                                                                                                                                                                                                        2; Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 353;
25;
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Best Local Similarity 31.6%; Pred. No. 25;
Matches 12; Conservative 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 KVSIPTKALELMDMOTFKAGK -- FCNFNFTLERRILKY 47
                                                                                                                                                                                                                                                                                                                                                                                Score 52; DB 2; Pred. No. 19; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 DGFNSSKCGVAVFLQNSSLQIFGTQSFK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DGLLKANCGMKVSIPTKALELMDMQTFK 29
                                                                                                                                                                                                                                                                                                                                                                                        21.1%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 32.1
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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F;591-609/Domain: transmembrane #status predicted <TM2>
F;620-638/Domain: transmembrane #status predicted <TM3>
F;630-638/Domain: transmembrane #status predicted <TM3>
F;805-825/Domain: transmembrane #status predicted <TM4>
F;1805-825/Domain: transmembrane #status predicted <TM4>
F;1805-820, 272, 286, 323, 408, 415, 479, 951/Binding site: carbohydrate (Asn) (covalent) #statu F;569, 663, 686, 725/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kiname F;655, 705/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kiname II) #
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NiAlternate names: Kainate receptor Kal
C;Spates: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: JS0685; S18266; S19154
C;Accession: JS0685; S18266; S19154
C;Accession: JS0685; S18266; S19154
A;Herb, A.; Burnashev, N.; Werner, P.; Sakmann, B.; Wisden, W.; Seeburg, P.H.
Neuron 8, 775-785, 1992
A;Title: The KA-2 subunit of excitatory amino acid receptors shows widespread expression:
A;Reference number: JH0592; MUID:92232306; PMID:1373632
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A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosiques: 1-956 <HER>
A;Cross-references: UNIPROT:Q01812; EMBL:X59996; NID:g57614; PIDN:CAA42615.1; PID:g57615.
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Nature 351, 742-744, 1991
A;Title: Cloning of a putative high-affinity kainate receptor expressed predominantly in A;Reference number: S18266; MUID:91287798; PMID:1648176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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C;Superfamily: glutamate receptor; glutamate receptor homology
C;Keywords: neurotransmitter receptor; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>F;21-956/Product: glutamate receptor chain KA-1 #status predicted
F;420-838/Domain: glutamate receptor homology <GRH>F;440-838/Domain: transmembrane #status predicted <AML>F;547-566/Domain: transmembrane #status predicted <AML>F;547-566/Doma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 52; DB 2; Length 956;
Pred. No. 71;
7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.1%; Score 22,
33.3%; Pred. No. 71;
ive 7; Mismatches 19; Indels
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OM protein - protein search, using sw model

August 1, 2005, 22:04:01; Search time 16.7062 Seconds (without alignments) 1088.086 Million cell updates/sec Run on:

US-09-489-079-28 Title: Perfect score:

246

1 KDGLLKANCGMKVSIPTKAL.....FKAGKFCNFNFTLERRILKY 47 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* A Geneseq 16Dec04:* Database

geneseqp20018:* geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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:	aci	pro	bre	pro	aci	bre	apl	bre	bre	tum	bre	bre	bre	gb]	bre										
e o	Amino	Human	Amino	Human	B726P	Human	Human	Human	Human	Human	Human	B726P	Нишап												
Description	Aab07642	Aab63909	Aab63906	Aab63926	Aab63933	Aab63929	Aab63918	Aab63937	Aab63917	Aab63903	Aab63901	Aab63925	Adb83983	Aab63899	Aab07638	Aab50249	Aag65987	Aau33350	Abg78917	Abj37740	Ad193135	Ade44425	Aab50263	Aag65983	Aau33346
QI	AAB07642	AAB63909	AAB63906	AAB63926	AAB63933	AAB63929	AAB63918	AAB63937	AAB63917	AAB63903	AAB63901	AAB63925	ADB83983	AAB63899	AAB07638	AAB50249	AAG65987	AAU33350	ABG78917	ABJ37740	ADL93135	ADE44425	AAB50263	AAG65983	AAU33346
BB	е	4	4	4,	4	4	4	4	4	4	4	4	7	ず	m	4	4	4	ß	9	7	œ	4	4	4
% Query Match Length	47	168	169	174	185	189	195	207	220	223	225	229	241	266	398	445	445	445	. 445	445	445	445	650	650	650
% Query Match	100.0	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8	61.8
Score	246	152	152	152	152	152	152	152	152	152	152	152	152	152	152	152	152	152	152	152	152	152	152	152	152
Result No.		8	ю	4	ß	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

	Abg78924 Human bre Abj37747 Human tum
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650 650 650 650 661 743 743 743 743 1002 1002 1002 1002 1003 1013 1013	1095
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152 152 152 152 152 152 152 152 152 152	152
77777777777777777777777777777777777777	44 5 45

ALIGNMENTS

Amino acid sequence of an antigenic peptide from BS322 polypeptide. Cohen M, Colpitts TL, Friedman PN, Gordon J; 28 SC, Klass MR, Kratochvil JD, Russell JC; BS322; breast tissue marker; breast disease; breast cancer. AAB07642 standard; peptide; 47 AA 21-JAN-2000; 2000WO-US001452. 99US-00234716. (first entry) Billing-Medel PA, Cohen I Granados EN, Hodges SC, Stroupe SD; WPI; 2000-499217/44. (ABBO) ABBOTT LAB. WO200043420-A1. Homo sapiens. 21-JAN-1999; 07-NOV-2000 27-JUL-2000. AAB07642; RESULT 1

BS322-specific polynucleotides, polypeptides and antibodies, used in the detection and diagnosis of breast disease especially breast cancer.

Claim 23; Page 125; 126pp; English.

The present sequence represents an antigenic peptide derived from human BS322 polypeptide. The peptide is used to raise antibodies. BS322 is a breast tissue marker. The BS322 polymucleotides and polypeptides are used to detect and diagnose breast disease, e.g. breast cancer. The BS322 polymucleotides are useful as a source of probes and primers, and the BS322 polypeptides are useful as antigens

Sequence 47 AA;

ö Gaps ö Ouery Match 100.0%; Score 246; DB 3; Length 47; Best Local Similarity 100.0%; Pred. No. 1.6e-28; Matches 47; Conservative 0; Mismatches 0; Indels

AAB63909 RESULT

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represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

Prostate cancer associated antigen precursors (CAAP) respectively.

AABG3232 to AABG3467, AABG3468 to AABG3721 and AABG3722 to AABG3970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate cancer associated antigen protein sequence SEQ ID NO:1288.
                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
             Human, breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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100.0%; Pred. No. 6e-14;
iive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB63926 standard; protein; 174 AA.
                                                                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                     26-MAY-2000; 2000WO-US014749.
                                                                                                                                                                                                                        99US-0136526P.
99US-0153454P.
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99US-0153454P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.8
Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-025274/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 169 AA;
                                                                                                            WO200073801-A2
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                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-1999;
10-SEP-1999;
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                                                                                                                                                 0.7-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nuclectide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate cancer associated antigen protein sequence SEQ ID NO:1268.
                                                                                                                                                                                                                                              Human prostate cancer associated antigen protein sequence SEQ ID NO:1271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                 Human, breast cancer, gastric cancer, prostate cancer, diagnosis,
cancer associated antigen, cytostatic, cancer vaccine.
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47
               Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.8%; Score 152; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                AAB63909 standard; protein; 168 AA
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99US-0153454P.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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10-SEP-1999;
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cancer.

AAB63906

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Gaps

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AAF22422 to AAF22656, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precureons (CAAP) respectively.

AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB633970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAP8 have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for disgnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate cancer associated antigen protein sequence SEQ ID NO:1291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
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                                                                                                                                                                                                                                                                                    Score 152; DB 4; Length 185;
Pred. No. 6.7e-14;
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                                                                                                                                                                                                                                                                                                    100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                         1 KDGLLKANCGMKVSIPTKALBLMDMQTFKA 30
                                                                                                                                                                                                                                                                                                                                                                                                    46 KDGLLKANCGMKVSIPTKALELMDMQTFKA 75
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                                                                                                                                                                                                                                                                                           61.8%;
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                                                                                                                                                                                                                                                                                                                                   30; Conservative
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                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                Sequence 185 AA;
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                                                                                                                                                                                                          e.g. cancer
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                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63123 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
represent human breast, gastric and prostate CAAP protein sequence respectively. CAAP8 have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
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                                                                                                                                                             Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                 AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.8%; Score 152; DB 4; Length 174; 100.0%; Pred. No. 6.2e-14;
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                                                                                                                                                                                                                                                                      Example 1; Page 779; 799pp; English.
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                                 (LUDW-) LUDWIG INST CANCER RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KDGLLKANCGMKVSI
                                                                                                                    WPI; 2001-025274/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-025274/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 174 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-2000
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                                                                          Obata Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer.
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Matches

RESULT 7 AAB63918

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AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63222 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                        Human prostate cancer associated antigen protein sequence SEQ ID NO:1299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate cancer associated antigen protein sequence SEQ ID NO:1279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                           Human, breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, breast cancer, gastric cancer, prostate cancer, diagnosis, cancer associated antigen, cytostatic, cancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 152; DB 4; I Pred. No. 7.6e-14;
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100.0%; Pred. No. '...
'... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 783-784; 799pp; English.
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                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                 99US-0136526P.
99US-0153454P.
                                                                                                                                                                                                                                             26-MAY-2000; 2000WO-US014749.
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     26-MAR-2001 (first entry)
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tes 30; Conserv
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                                                                                                                                                                       WO200073801-A2.
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                                                                                                                                                                                                                                                                                   28-MAY-1999;
                                                                                                                                                                                                                                                                                                     10-SEP-1999;
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                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer.
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AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                     Human prostate cancer associated antigen protein sequence SEQ ID NO:1280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                          Gaps
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                                                                                                                                                                                                                                                                                                                                         Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
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                         Indels
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100.0%; Prec. ...
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                                                                                                KDGLLKANCGMKVSIPTKALELMDMQTFKA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 775-776; 799pp; English
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                                                                                                                                                                                          AAB63918 standard; protein; 195 AA
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100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0136526P.
99US-0153454P.
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                                                                                                                                                                                                                                                                  (first entry)
                         30; Conservative
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Matches 30; Conserv
     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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10-SEP-1999;
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                                                                                                                                                                                                                               AAB63918;
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cancer

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Gaps

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26-MAY-2000; 2000WO-US014749.

AAB63937

RESULT 8 AAB63937

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Gaps

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Obata Y;

cancer.

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represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63122 to AAB63467, AAB63468 to AAB63721 and AAB63122 to AAB63467, AB63468 to AAB63721 and AAB63122 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAP6 have cytostatic activity and can be used in the production of cancer vaccines. The human CAPP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for disgnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                   AAF22422 to AAF22656, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63222 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPS have cytostatic activity and can be used in the production of cancer vaccines. The human CAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate cancer associated antigen protein sequence SEQ ID NO:1263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
                                                                                                                                                                                                                                                                                                                                                 61.8%; Score 152; DB 4; Length 223;
100.0%; Pred. No. 8.4e-14;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KDGLLKANCGMKVSIPTKALBLMDMQTFKA 30
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                Example 1; Page 769; 799pp; English.
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99US-0153454P.
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                                                                                                                                                                                                                                                                                                                                                                                               30; Conservative
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                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                         Sequence 223 AA;
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10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-2000.
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                                                                                                                                                                                                                                                                  e.g. cancer
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                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                        AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63467, AAB63467 and AAB63721 and AAB63722 to AAB63467, AAB63467 and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate cancer associated antigen protein sequence SEQ ID NO:1265.
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                                                                                                                                                                                                                   Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
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Local Similarity 100.0%; Pred. No. 8.2e-14;
nes 30; Conservative 0; Mismatches 0;
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                                                                                      (LUDW-) LUDWIG INST CANCER RES
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                    99US-0136526P.
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                                                                                                                                                                            WPI; 2001-025274/03:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 220 AA;
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                    28-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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26-MAR-2001

AAB63903;

RESULT 10 AAB63903

Query Match

Best Loc Matches

ઠ 셤 07-DEC-2000

Obata Y;

Matches

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RESULT 12

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AAB63925

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The invention related to a combination of polynucleotides. The combination of polynucleotides is useful for preparing a composition for diagnosing or treating cancer or neurodegenerative disorders. The present sequence represents the amino acid sequence of the human breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New combination of polynucleotides, useful for preparing a composition for diagnosing or treating cancer or neurodegenerative disorders.
                                                                                    Human breast cancer diagnostic marker protein Incyte 411152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.8%; Score 152; DB 7; Length 241; Best Local Similarity 100.0%; Pred. No. 9.2e-14; Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                     cancer; neurodegenerative disorder; human; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 KDGLLKANCGMKVSIPTKALELMDMQTFKA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KDGLLKANCGMKVSIPTKALELMDMQTFKA 30
                                                                                                                                                                                                                                                                              by GAT"
                                                                                                                                                                                                                                                                                                               by AAT"
                                                                                                                                                                                                                                                                                                                                                                                  'note= "Encoded by CCC"
                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Encoded by AGA"
                                                                                                                                                                                                                                            /note= "Encoded by GAG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 11; Page 20-21; 22pp; English.
                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 note= "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ź
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                                                                                                                                                                                                                                                                                                                 'note= "Encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB63899 standard; protein; 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walker MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2002; 2002US-00133757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-APR-2001; 2001US-0287153P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2001 (first entry)
                                                  04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-687833/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mahini B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZHAN/) ZHANG C.
(MAHI/) MAHINI B.
(WALK/) WALKER M G.
                                                                                                                                                                                                                                                                                                                                 Misc-difference 79
                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 83
                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 85
                                                                                                                                                                                                                                                            Misc-difference 75
                                                                                                                                                                                                                                                                                               Misc-difference 76
                                                                                                                                         diagnostic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADB83986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 241 AA;
                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2003104418-A1
                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB63899;
                  ADB83983;
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AAB63899
ID AAB63
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AC AAB63
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AAB62232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
                                                                                                                                                                                                                                                                                                                                   Human prostate cancer associated antigen protein sequence SEQ ID NO:1287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                   Human, breast cancer, gastric cancer, prostate cancer, diagnosis, cancer associated antigen, cytostatic, cancer vaccine.
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                                    Length 225;
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                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                  Score 152; DB 4; I
Pred. No. 8.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.8%; Score 152; DB 4; 100.0%; Pred. No. 8.7e-14; ive 0; Mismatches 0;
                     61.8%; Sco...
100.0%; Pred. No. c...
0; Mismatches
                                                                                                                          91 KDGLLKANCGMKVSIPTKALELMDMQTFKA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 KDGLLKANCGMKVSIPTKALELMDMQTFKA 137
                                                                                                      30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KDGLLKANCGMKVSIPTKALELMDMQTFKA 30
                                                                                                     1 KDGLLKANCGMKVSIPTKALELMDMQTFKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 778-779; 799pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB83983
ID ADB83983 standard; protein; 241 AA.
                                                                                                                                                                                                                              Ā
                                                                                                                                                                                                                            AAB63925 standard; protein; 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000; 2000WO-US014749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0136526P.
                                                                                                                                                                                                                                                                                                (first entry)
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-025274/03.
                                                  Local Similarity
Les 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 229 AA;
Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200073801-A2
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-DEC-2000
                                                                                                                                                                                                                                                                                                26-MAR-2001
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                                                                                                                                                                                                                                                            AAB63925;
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                                  Query Match
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Gaps

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Matches

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76 KDGLLKANCGMKVSIPTKALELMDMQTFKA 105
                                                                                                                                                                                                                                                                                                                                     1 KDGLLKANCGMKVSIPTKALELMDMQTFKA 30
                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: August 1, 2005, 22:18:05 Job time : 17.7062 Bec8
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 30; Conservative
(ABBO ) ABBOTT LAB.
                                      Granados EN,
                                                 Stroupe SD;
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                                                                                                                                                                                                                                                                                                                                                                         represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63322 to AAB63463, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and creating a condition characterised by expression of an abnormal amount of a protein,
 Human prostate cancer associated antigen protein sequence SBQ ID NO:1261.
                                                                                                                                                                                                                                                                                   Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                         Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.8%; Score 152; DB 4; Length 266; 100.0%; Pred. No. 1e-13; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BS322; breast tissue marker; breast disease; breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 61.8%; Score 152; DE
Best Local Similarity 100.0%; Pred. No. 1e-
Matches 30; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KDGLLKANCGMKVSIPTKALELMDMQTFKA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of BS322 polypeptide.
                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 767; 799pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB07638 standard; protein; 398 AA
                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-2000; 2000WO-US001452
                                                                                                                                                                     99US-0136526P.
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                                                                                                                                           26-MAY-2000; 2000WO-US014749
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                                                                                                                                                                                                                                                           WPI; 2001-025274/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200043420-A1
                                                                                          WO200073801-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                 Homo sapiens.
                                                                                                                                                                     28-MAY-1999;
10-SEP-1999;
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                                                                                                                    07-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB07638;
                                                                                                                                                                                                                                     Obata Y;
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The present sequence represents a human BS322 polypeptide. BS322 is a breast tissue marker. The BS322 polymucleotides and polypeptides are used to detect and diagnose breast disease, e.g. breast cancer. The BS322 polymucleotides are useful as a source of probes and primers, and the BS322 polypeptides are useful as antigens
                                                                                                                                                                                                                                                                                                      BS322-specific polynucleotides, polypeptides and antibodies, used in the detection and diagnosis of breast disease especially breast cancer.
PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
Hodges SC, Klass MR, Kratochvil JD, Russell JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 23; Page 122-123; 126pp; English.
                                                                                                                                                                              WPI; 2000-499217/44.
    Billing-Medel PA,
                                                                                                                                                                                                                            N-PSDB; AAA59015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 398 AA;
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Gaps

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61.8%; Score 152; DB 3; Length 398; 100.0%; Pred. No. 1.7e-13; ive 0; Mismatches 0; Indels

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(without alignments) 1831.334 Million cell updates/sec August 1, 2005, 22:05:16 ; Search time 13.1422 Seconds US-09-489-079-28

Run on:

246 1 KDGLLKANCGMKVSIPTKAL.....FKAGKFCNFNFTLERRILKY 47 Perfect score: Sequence:

1612378 seqs, 512079187 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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	į		homo sapien	homo sapien	drosophila	clostridium		_		-	carassius a	-		_	bacteroides	phoca vitul	streptococc	streptococc	equus cabal	thermotoga	daucus caro	homo sapien	bacillus ha	homo sapien	homo sapien	_	• •		schizosacch	homo sapien	neurospora	bacteroides	listeria mo
	40,140,000	di incenti	Q9bxx3	Q9bxx2	Q9v£26	Q97fr1	026453	Q6ij09	07sgm9	Q6fwk3	093552	Q70ut1	08juv0	Q726u0	Q6a564	06pud2	Q8e1j9	Q8e716	028386	051933	Q94829	O9nwe9	Q9ke87	09h1q1	Ognba8	Q6cpi8	Q92jq4	07pac1	094415	Q96dn3	92n960	Q64z91	Q8y852
SUMMARIES	ţ	TD	Q9BXX3	Q9BXX2	Q9VF26	Q97FR1	026453	Q61J09	Q7SGM9	Q6 FWK3	093552	Q70UT1	QBJUV0	Q726U0	Q6A564	Q6PUD2	Q8E1J9	Q8E716	IL1B_HORSE	SAHH_THEMA	Q94S29	O9NW69	Q9KE87	Q9H1Q1	Osupse	Q6CP18	Y013 RICCN	Q7PAC1	SUCB_SCHPO	096D <u>N</u> 3	Q96UC6	064291	Q8Y852
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,	Query	March	61.8	48.0	26.8	26.2	26.0	24.6	24.4	24.4	24.0	23.6	23.4	23.2	23.2	23.0	22.6	22.6							22.4		22.0	22.0	22.0	22.0	21.7	21.7	21.5
		Score	152	118	99	64.5	64	60.5	9	9	59	58	57.5	57	57	56.5	55.5	55.5	55.5	55.5	55	55	55	55	55	54.5	54	54	54	54	53.5	53.5	53
	Result	. i		7	m	4	Ŋ	9	7	60	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	. 24	25	26	27	28	29	30	31

Q721a4 listeria mo Q72vx0 leptospira Q8f9j0 leptospira	Q9htp4 pseudomonas Q6u6h0 oat necroti Q96rw7 homo sapien	Q8pp02 xanthomonas Q66d48 yersinia ps Q8zqv4 yersinia pe	Q899aO phaseolus a Q6f2b3 mesoplasma Q64r18 bacteroides	
Q721A4 Q72VX0 Q8F9J0	Q9HTP4 Q6U6H0 Q96RW7	Q8PP02 Q66D48 Q8ZGV4	Q8S9A0 Q6F2B3 Q64RL8	Q92TS0 081838
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ALIGNMENTS

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                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Breast cancer antigen NY-BR-1.
Homo sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                     Length 1341;
                                                                                                                                                                                                                                                                                                                                     1341 AA; 152776 MW; 33E53DDE6FD3A58B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-UNN-2001 (TrEMBLrel:-17,-Créated)
01-UNN-2001 (TrEMBLrel: 17, Last sequence update)
01-UNN-2003 (TrEMBLrel: 24, Last annotation update)
Breast cancer antigen NY-BR-1:1 (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                            /1011 AA.
                 PRT; 1341 AA.
                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50088; ANK REPEAT; 4.
PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                            1 KDGLLKANCGMKVSIPTKALELMDMQTFKA 30
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                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 30; Conserva
                                                                                                    NCBI_TaxID=9606;
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SEQUENCE
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                             09BXX3
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                   Q9BXX3
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Q9BXX2
ID Q9BXX
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OS HOMO
RESULT 1
Q9BXX3
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer E.E., Li P.W., Hookins K.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yachards S., Ashburner M., Henderson S.N.,
R.A. Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
R.A. Abril J.F., Apbayani A., An H.J., Andrews-Ffannkoch C., Baldwin D.,
R.A. Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
R. Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.S., Buller H., Cadieu E., Center A., Chandra I.,
R. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
R. Borkova D., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A delan K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
R. Honden N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
A Harris N.L., Harvey D., Heiman T.J., Wellen, M.M., Classer K.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kannison J.R., Ketchum K.A.,
Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
A Harkulov G., Milshina N.V., Mobarry C., Morris J., Mopherson D.L.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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                                                                             Jaeger D., Stockett E., Guere A.O., Scanlan M.J., Karbach J.,
Jaeger E., Knuth A., Old L.J., Chen Y.T.;
Jaeger E., Knuth A., Old L.J., Chen Y.T.;
Identification of a Tissue-specific Putative Transcription Factor in
Breast Tissue by Serological Screening of a Breast Cancer Library.";
Cancer Res. 61:2055-2061(2001).
EMBL, AP269088, AAXZ7326.1;
InterPro; IPR002110; ANK.
InterPro; IPR002110; ANK.
SMART; SM00248; ANK, 3.
PROSITE; PS50088; ANK REPEAT; 1.
PROSITE; PS50089; ANK REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                  Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa; Arthropoda, Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                      Length 1011;
                                                                                                                                                                                                                                                                           1011 AA; 114250 MW; 16627D7B218DE438 CRC64;
                                                                                                                                                                                                                                                                                                                                  Indels
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Last annotation update)
                                                                                                                                                                                                                                                                            114250 pm,
48.0%; Score 118; DB 2; Le
78.0%; Pred. No. 9.6e-08;
5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                          SEQUENCE FROM N.A.
MEDLINE=21174979; PubMed=11280766;
                                                                                                                                                                                                                                                                                                                   Local Similarity 73.3%;
nes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=spn-E; ORFNames=CG3158;
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Q9VF26
ID Q9VF3
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R GO; GO:0005737; C:cytoplasm; NAS.

R GO; GO:0005737; C:cytoplasm; NAS.

R GO; GO:0005737; C:cytoplasm; NAS.

R GO; GO:0008724; F:RNA helicase activity; TAS.

R GO; GO:0008298; P:RATOGRALID silencing; IMP.

R GO; GO:0007294; P:RATOGRALICATION, INTRAcellular; IMP.

R GO; GO:0007294; P:OCOYTE GALLATION; IMP.

R GO; GO:00073072; P:COCYTE DOSILIONING; IMP.

R GO; GO:0009949; P:POLarity specification of anterior/posterio. .; IMP.

R GO; GO:0007315; P:POLarity specification of dorsal/ventral axis; IMP.

R GO; GO:0007315; P:POLe plasm assembly; NAS.

R GO; GO:0007317; P:regulation of pole plasm oskar mRNA localiz. .; IMP.

R GO; GO:0007317; P:regulation of pole plasm oskar mRNA for des. .; IMP.

R GO; GO:0007317; P:Regulation of Pole plasm oskar mRNA for des. .; IMP.

R InterPro; IPRO1140; DEAD.

R InterPro; IPRO11550; Helicase_C.
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Shen E.C., Sidenington K., Saunders R.D., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Svirsks R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang S.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Zhong F.N., Zhong W., Zhou C., Zheng L., Zheng K.H., Zhong F.N., Zhong W., Zhou C., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJINE-2245065; PubMed=12537568;
MEDIJINE-2245065; PubMed=12537568;
MEDIJINE-2245065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patifer B.D., Richards S., Sodergren E.J., Weinskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a Wolce-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.",
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MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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EMBL; AE003710; AAF55235.1; -.
FlyBase; FBgn0003483; spn-E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 287:2185-2195(2000).
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Pfam;

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GO:0005737; C:cytoplasm; NAS.
GO:0003724; F:RNA helicase activity; TAS.
GO:0003724; F:RNA helicase activity; TAS.
GO:0003724; F:Chromatin silencing; IMP.
GO:000399; P:Chromatin silencing; IMP.
GO:0007294; P:Occyte cell fate determination (sensu Insecta); IGI.
GO:0007294; P:Occyte maturation; IMP.
GO:0007295; P:Occyte maturation; IMP.
GO:000951; P:Occyte positioning; IMP.
GO:0009949; P:polarity specification of anterior/posterio. .; IMP.
GO:000951; P:polarity specification of dorsal/ventral axis; IMP.
GO:0007315; P:polarity specification of corsal/ventral axis; IMP.
GO:0007317; P:regulation of pole plasm oskar mRNA localiz. .; IMP.
GO:0003423; P:RNA interference, targeting of mRNA for des. .; IMP.
                                                                                                                                                                                                                                                             Gillespie D.E., Berg C.A.;
"Homeless is required for RNA localization in Drosophila cogenesis and encodes a new member of the DE-H family of RNA-dependent ATPases.";
Genes Dev. 9:2495-2508(1995).
EMBL; S79915; AAB35476.2; -.
PIR; T13889; T13889.
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;

Eukaryota, Badoptera, Diptera; Brachycera; Muscomorpha;

Ephydroidea, Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                        Drosophila sp. (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1441;
                                                    Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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ATP-binding; Helicase; Hydrolase.
SEQUENCE 1441 AA; 164980 MW; 5B52C1666C99347E CRC64;
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Last annotation update)
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Pred. No. 8.6;
7; Mismatches 19
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PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;
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InterPro; IPR001650; Helicase C.
InterPro; IPR007505; Helicase dom.
InterPro; IPR00191; Maternal_tudor.
InterPro; IPR002999; Tudor.
                                                                                                                                                                                                         STRAIN=Canton-S; TISSUE=Ovaries; MEDLINE=96033800; PubMed=7590230;
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Ppfam; PP00567; TUDOR; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
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33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001410; DEAD
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Pfam; PF04408; HAZ; 1.
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Best Local Similarity
                                                                                                                                                                                   SEQUENCE FROM N.A.
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Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibbon R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stam L.A., Soucaille P.,
Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMBL, AE007764; AAK80613.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=CAC2666;
Clostridium acetobutylicum.
Bacteria; Pirmicutes; Clostridia; Clostridiales; Clostridiaceae;
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26.2%; Score 64.5; DB 2; Length 461;
Best Local Similarity 45.7%; Pred. No. 2;
Matches 16; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 1434;
                                                                                                                                                                                                                                                                                                               PROSITE; PSS0304, TUDOR; 1.
PROSITE; PSS0304, TUDOR; 1.
ATP-binding; Helicase; Hydrolase.
ASPOROUSE 1.1434 AA, 164509 MW; 67E8CD39F1484B13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome; Hypothetical protein.
SEQUENCE 461 AA; 54132 MW; AC320839BE059C03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 KANCGMKVSIPTKALELMDMQTFKAGKFCNFNFTLERRI 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CAC2666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
  InterPro; IPR007502; Helicase_dom.
InterPro; IPR008191; Maternal_tudor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                        InterPro; IPR008191; Maternal_
InterPro; IPR002999; Tudor.
InterPro; IPR007087; Znf_C2H2.
                                                                                                                                                                                                         SMART; SM00487; DELLC; 1.
SMART; SM00490; HELICC; 1.
SMART; SM00333; TUDOR; 1.
SMART; SM00355; ZMP CZH2; 1.
                                                                                                                                 PF04408; HAZ; 1.
PF00271; Helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.8%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 01, TrEMBLrel. 01, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                     PF00567; TUDOR; 1
                                                                                                        Pfam; PF00270; DEAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; B97228; B97228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (
01-NOV-1996 (
01-MAR-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium
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Q26453;
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097FR1; **Q97FR1**

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RESULT 5 026453

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Q6FWK3
Q6FWK3;
05-JUL-2004 (
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      093552
093552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                    HIDDEN SOON OF THE PROPERTY OF
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Galagan J. B., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., A Galagan J. B., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., A Jaffe D., Fitzhugh W., Man L.-J., Smirnov S., Purcell S., Rehman B., Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Roth G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Krystoffova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Araden O., Plamann M., Seller S., Dunlap J., Nedford A., Aramayo R., Yarden O., Plamann M., Seller S., Dunlap J., Radford A., Aramayo R., Matvig D.O., Alax L.A., Mannhaupt G., Ebbole D.J., Freiteg M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.; The Genome Sequence of the Filamentous Fungus Neurospora crassa.;

I. Nature O. D.O. (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- CAUTION: The sequence shown here is derived from an preliminary data.

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AABXO1000009; EAA35949.1; -.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . .; IEA. GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR001764; Glyco hydro_3N.

PRINTS; PR00133; GLHYDRLASE3.
Hild M., Beckmann B., Haas S., Koch B., Solovyev V., Busold C., Fellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J., Paro R.; "An integrated gene annotation and transcriptional profiling approach towards the full gene content of the Drosophila genome."; Genome Biol. 5:R3-R3(2003).
-!- MISCELLANEOUS: The sequence shown here is derived from an EMBL/Genbank/DDBJ third party annotation (TPA) entry.
EMBL; BK002907; DAA04412.1; ...
SEQUENCE 160 AA; 18064 MW; E7D5FFA10221CA36 CRC64;
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                                                          14; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 160;
                                                                                                                                                                                                                                                                                                                                                              1 KDGLLKANCGMKVSIPTKALELMDMQTFKAGK------FCNFN 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.4%; Score 60; DB 2; Length 980; 39.0%; Pred. No. 21; ive 2; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               980 AA; 106688 MW; EEEDOC9AB17C7048 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                           24.6%; Score 60.5; Di
29.2%; Pred. No. 2.3;
tive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         980 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                    Query Match
Best Local Similarity 29.4.
Best Local 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 39.09
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=NCU08054.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
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RESULT 8

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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Roffard N., Prangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Rarnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Roper G., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztes S., Ozier-Kalogeropoulos O.,
Nicaud J.M., Nikolski M., Oztes S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekata F., Wesolowski-Louvel M., Westhof B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Mincker P., Souciet J.L.;
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In Nature 430:35-44(2004).

In SIMILARITY: Belongs to the Ser/Thr protein kinase family.

In GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:ATP binding; IEA.

GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.

GO; GO:0006468; F:protein serine/threonine kinase activity; IEA.

GO; GO:0006468; F:protein amino acid phosphorylation; IEA.

InterPro; IPR000719; F:ATP kinase.

InterPro; IPR002290; Ser_thr_pkinase.

InterPro; IPR00245; Tyr_pkinase.

InterPro; IPR00159; Fire Pykinase.

InterPro; IPR00159; Fire Pykinase.

InterPro; IPR00169; Fire Pykinase.

InterPro; IPR00169; Fire Pykinase.

InterPro; IPR00169; Fire Pykinase.

InterPro; IPR00169; Fire Pykinase.
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SWART; SW00220; S_TKC; 1.
SWART; SW00219; TYRC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine,threonine-protein kinase; Transferase.
SEQUENCE 1076 AA; 122681 MM; B3F1FE037A16B126 CRC64;
                                                                                                                                                                                                                                       Candida glabrata CBS138.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGLLKA------NCGMKVSIPTKALELMDMQTFKAGKFCNFNFTLE 41
                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
85-Millar to sp|P276 Saccharomyces cerevisiae YAR019c CDC15.
ORFNames=CAGLOC05005g;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       844 AA
PRT; 1076 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative odorant receptor.
Name=GFB1;
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   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=284593;
                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CBS138;
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01-NOV-1998 (
01-MAR-2004 (
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Gaps

18;

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1005 SSPIPSLELMYITSYRFYQRIYEVLSWFCKDNKKCGKFCNFICAIWGYLREKGLLIF 1061
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Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marco C.F., Aguilar J.M., Abad J., Gomez-Guillamon M.L., Aranda M.A.; Submitted (PEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, 3X242071, AAM7368-2; ---
EMBL, A2X242077; AAM7368-2; ---
GO, GO:000174; F:RNA methyltransferase activity; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003724; F:RNA helicase activity; IEA.
GO; GO:00036396; F:RNA helicase activity; IEA.
GO; GO:0006396; F:RNA processing; IEA.
GO; GO:0019079; P:viral genome replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 SIPTKALBLMDMQTF-----KAGKFCNF----NFTLERRILKY 47
                                                                                                                                                                                                                                                                                                                                                                            463 1979 methyltransferase/helicase-like protein.
1980 2483 RNA-dependant RNA polymerase.
1 462 putative leader proteinase.
2483 AA; 286168 MW; 0F56A44058407C84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=22799014; PubMed=12917477; DOI=10.1099/vir.0.19209-0; Agullar J.M., Franco M., Marco C.F., Berdiales B., Rodriguez-Cerezo E., Truniger V., Aranda M., Franca M., Futcher variability within the genus Crinivirus, as revealed by determination of the complete RNA genome sequence of Cucurbit yellow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 NCGMKVSIPTKALELMDMQTF-------KAGKFCNF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 2; Lengtn 440.7 Pred; No. 1.2e+02;
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Pred. No. 1.1e+02;
8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0019079; P:viral genome replication; IEA.
InterPro; IPR002160; Prot inh Kunz-1g.
InterPro; IPR002566; Viral helicasel.
InterPro; IPR002588; V methyltrans.
Pfam; PF01443; Viral helicasel; 1.
Pfam; PF01660; Vmethyltransf; 1.
PROSITE; PRO1660; Vmethyltransf; 1.
PROSITE; PRO1683; SOYBEAN KUNITZ; UNKNOWN 1.
SEQUENCE 1977 AA; 2268IZ MW; CFD290023EA10CDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
   InterPro; IPR001038; RNA_dep_RNApol2.
InterPro; IPR007094; RNA_pol_DS_PS.
InterPro; IPR007094; RNA_pol_DS_VI.
InterPro; IPR007094; Viral_helicasel.
InterPro; IPR005588; V_methyltrans.
Pfam; PF00978; RNA_dep_RNApol2; 1.
Pfam; PF01443; Viral_helicasel; 1.
Pfam; PF01660; Viral_helicasel; 1.
PR05ITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stunting disorder virus.";
J. Gen. Virol. 84:2555-2564(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.4%;
Local Similarity 28.1%;
hes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 31.9
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=51330;
                                                                                                                                                                                                                                                                                                                                                                                                                              1980
                                                                                                                                                                                                                                                                                                                                                     Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crinivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBJUVO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08JJV0
                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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                   셤
                                                                                                                                                                                                                                                                   MEDINE-9842655; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;

MEDINE-98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;

MEDINE-98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;

MEDINE-98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;

MEDINE-98426265; PubMed=9751777; DOI=10.1073/pnas.95.20.11987;

MEDINE-9842667; PubMed=10calization of two multigene receptor families in goldfish olfactory epithelium.";

MEDINE-9842667; Preceptor epithelium.";

MEDINE-9842667; Preceptor activity; IEA.

MEDINE-9842667; Preceptor activity; IEA.

MEDINE-984267; Preceptor activity; IEA.

MEDINE-984267; Preceptor activity; IEA.

MEDINE-984267; Preceptor activity; MEA.

MEDINE-984267; Preceptor activity; MEA.

MEDINE-984267; PRO10337; GPCR.

METER-PRO; IPRO10337; MARCINE-984267.

METER-PRO; IPRO10337; VATON-RECEPTOR:

METER-PRO; IPRO1034; VATON-RECEPTOR:

METER-PRO; IPRO1034; ANF-RECEPTOR:

METER-PROPORTINE ANF-RECEP
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Viruses; SeRNA positive-strand viruses, no DNA stage; Closteroviridae;
Crinivirus.
Actinopterygii; Neoptergii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Carassius.
NCBI TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Coutts R. H.A., Livieratos I.C.;

"Nucleotide sequence and genome organisation of Cucurbit yellow
I stunting disorder virus RNAL.";

Arch. Virol. 148:2055-2061(2003).

EMBL; AJ537493; CAD61026.2; -...

R GO; GO:0008174; F:RNA methyltransferase activity; IEA.

R GO; GO:0003724; F:RNA binding; IEA.

R GO; GO:0003724; F:RNA binding; IEA.

R GO; GO:000368; F:RNA directed RNA polymerase activity; IEA.

R GO; GO:0006396; F:RNA processing; IEA.

R GO; GO:0006396; P:RNA processing; IEA.

R GO; GO:0006396; P:VANA genome replication; IEA.

R GO; GO:0009099; P:VIXAB genome replication; IEA.

R InterPro; IPR002160; Prot_inh_Kunz-1g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS00981; G PROTEIN RECEP F3 3; 1.
PROSITE; PS50259; G PROTEIN RECEP F3 4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 CGSRLSTMTATMGLMNSQDFGPGNICN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 CGMKVSIPTKALELMDMQTFKAGKFCN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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MEDLINE=22897980; PubMed=14551825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00248; GPCRMGR.
PRINTS; PR01535; VOMERONASL2R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 40...
Best Local 11; Conservative
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SEQUENCE
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PubMed=14761991; DOI=10.1128/JB.186.4.968-977.2004;
                                                                                                                                                J. Bacteriol. 186:968-977(2004).
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Pfam; PF00963; Cohesin; 10.
Pfam; PF00395; SLH; 3.
SMART; SM00183; NAT_PEP; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                             cellulase.
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SIGNAL
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X PubMed=15077118; DOI=10.1038/nbt959;

A Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
Heidelberg J.F., Seshadri R., Mard N.L., Methe B.A., Brinkac L.M.,
Kolonay J.F., Blsen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
A Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
A Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
A Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
A Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
A Peldblyum T.V., Wall J.D., Voordouw G., Praser C.M.;
T'The genome sequence of the anaerobic, sulfate-reducing bacterium
Desulfovibrio vulgaris Hildenborough.";
B EMBL; ABG17319; AAS97487.1;

R TIGR; DV03016;

T.T.
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                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio.
                                                                                                                                                                                                                              Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20398177; PubMed=10940036; DOI=10.1128/JB.182.17.4915-4925.2000; Doi=10.1128/JB.182.17.4915-4925.2000; Ding S.Y., Bayer B.A., Steiner D., Shoham Y., Lamed R.; Ding S.Y., Bayer E.A., Steiner D., Shoham Y., Lamed R.; Contains II type II cohesins."; J. Bacteriol. 182:4915-4925(2000).
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
NCBI_TaxID=35825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.2%; Score 57; DB 2; Length 481; Best Local Similarity 42.9%; Pred. No. 26; Matches 12; Conservative 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 AA; 54075 MW; 5A4FF907A7CBB263 CRC64;
                                                                                                                                                                          B12 binding domain protein/radical SAM domain protein.
OrderedLocusNames=DVU3016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Cellulosomal anchoring scaffoldin B precursor.
                                                                                                (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0050897; F:cobalt ion binding; IEA.
GO; GO:005506; F:iron ion binding; IEA.
InterPro; IPR006158; B12-binding.
InterPro; IPR006638; B1937MiaB/NifB.
InterPro; IPR006638; B1937MiaB/NifB.
Fam; PF02310; B12-binding; I.
PFam; PF02310; B12-binding; I.
PFam; PF02310; B12-binding; I.
PFam; PF04055; Radical SAM; I.
                                                    481 AA
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25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
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                                                    PRT;
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                                                    PRELIMINARY;
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SEQUENCE 481 AA
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=882;
                                                                                                   05-JUL-2004
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Q6A564;
RESULT 12
(07260)
DY 07260
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Q6A564

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Gaps
Xu Q., Bayer B.A., Goldman M., Kenig R., Shoham Y., Lamed R.; "Architecture of the Bacteroides cellulosolvens cellulosome: description of a cell surface-anchoring scaffoldin and a family 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phoca vitulina richardsi.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Pinnipedia, Phocidae, Phoca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 29 Potential.
30 2299 cellulosomal anchoring scaffoldin
2299 AA; 243625 WW; CAB441B67D4BFC2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                                                                                                                                                                                                  Lamed R.;
                                                                                                                                                                                                                                                           Xu Q., Bayer E. A., Goldman M., Kenig R., Shoham Y., Lamed R. Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF224509; AAT79550-11.

GO, GO:0002274; C:cell wall (sensu Bacteria); IEA.

GO, GO:0005779; C:cell wall (sensu Bacteria); IEA.

GO, GO:0005779; P:hormone activity; IEA.

GO, GO:0005779; P:polysaccharide catabolism; IEA.

InterPro; IPR008965; Cellul bind.
InterPro; IPR008965; Cellul bind.
InterPro; IPR008105; Cohesin.
InterPro; IPR00119; SiM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2299;
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                                                                                                                                                                     Ding S.-Y., Bayer E.A., Shoham Y., Steiner D., Lamed R. Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Interleukin-1 beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 23.2%; Score 57; DB 2; I
Best Local Similarity 28.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 8; Mismatches 20;
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SEROLYPE V;
STRAIN-2603 V/R / Serotype V;
MEDLINE-22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
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Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
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InterPro; IPR003294; InterleukinILIAB.
InterPro; IRR003296; InterleukinILIB.
InterPro; IPR00376; Interleukin_I.
Pfam; PR00340; ILI, 1.
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Pfam; PR00346; ILI, 1.
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PRINTS; PR01357; INTELLEUKINIB.
PRODOM; PR00125; ILI, 1.
PROSITE; SM00125; ILI, 1.
INFRAMATICHY II. 1.
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Bacteria; Pirmicutes; Lactobacillales; Streptococcaceae;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SAG0155.
OrderedLocusNames=SAG0355;
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Best Local Similarity 34.0%; Pred. No. 16;
Matches 17; Conservative 10; Mismatches
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NCBI_TaxID=216466;
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM protein - nucleic search, using frame plus p2n model	Run on: August 1, 2005, 22:44:18; Search time 1787.61 Seconds (without alignments) 1000.786 Million cell updates/sec	Title: US-09-489-079-28 Perfect score: 246 Sequence: 1 KDGLLKANCGMKVSIPTKALFKAGKFCNFNFTLERRILKY 47	Scoring table: BLOSUM62 Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0	Searched: 34239544 seqs, 19032134700 residues	Total number of hits satisfying chosen parameters: 68479088	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Command line parameters: -MODEL=frame+_pzn.model -DEV=xlp -Q=/cgn2_1/USPTO_spool_p/US09489079/runat_01082005_141250_13309/app_query.fasta_1.1635 -DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0	-UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE-ECC -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODB=LOCAL	-UGIFMI=PLO -NUKMPEKT -NEAPOILE=30 -NUMBER - "MANDEN=2000000000000000000000000000000000000	Database : EST:* 1: gb_est1:* 2: gb_est2:*	3: gp_nrc:* 4: gp_est4:* 5: gb_est4:*	6: gb_est5:* 7: gb_est6:* 8: gb_gss1:* 9: gb_gss2:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Query	Score Match Length DB ID Descript. 220.5 89.6 532 8 B17512 817512 3	220.5 89.6 665 8 B15703 B15703 3.168 68.3 685 9 AG010131 AG010131 AG010131 AG010132 AG010132	C 6 161.5 477 8 AG067184 AG067184 AG067184 BS_2109_A C 6 161.5 65.7 695 9 AG010124 AG010124 HOMD 88pi 7 152 61.8 514 5 BP312630 BP312630 BP312630 8 152 61.8 581 5 BP314667 BP314667 BP314667	152 61.8 582 5 BP313026 BF313026

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Matches:
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AG010131 AG003942
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Homo sapiens
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TITLE
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REFERENCE
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KEYWORDS
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Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 665)

Adams, M.D., Kelley, J.M., Rounsley, S.R. and Venter, J.C.
Use of a BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1997)

LOCATE GSSs: 345002.TPB 345002.TVB

Contact: Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
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/note="lab="DAGC108L; Site_1: HindIII; Site_2: HindIII;

CalTech Human BAC Library A1"
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Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
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db xref="taxon:9606"
/clone="A-345002"
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/cell type="Fibroblast"
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

The Common Second Common Common Common.

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21g

Leblished Only in DataBase (1998)

Leblished Only in Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (B-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel.:042-778-9321)

On Feb 5, 1999 this sequence version replaced gi:2760801.

AG003942: Submitted (09-Jan-1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AG010131 685 bp DNA linear GSS 14-APR-1999
Homo sapiens genomic DNA, 21g region, clone: £2G2X4, genomic survey
                                                                                                                                                                                                                                                                                                                                 94 TTTATGAAGTATACATTGTATATTGTTTTTTTTTCTTTCCAAACCCATTTAAGCTAACTGC 153
                                                                                                                                                                                                                                                                                    10 GlyMetLysValSerIleProThrLysAlaLeuGluLeuMetAspMetGlnThrPheLys 29
                                     34 AAAGATGGTCTTCTGAAAGTAATAACTTTTATATTTTTATCTTGAGTAGTAACTACATAT 93
9
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

FEATURES COMMENT

DEFINITION

AG010132

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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 477)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AG010124 695 bp DNA linear GSS 14-APR-1999
Homo sapiens genomic DNA, 21g region, clone: £2G2X4, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
7el: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2109 row: A column: 15
Seg primer: T?
Class: BAC ends
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 695)

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Homo sapiens genomic DNA, chromosome 21q

Published Only in DataBase (1998)

2 (Dases 1 to 695)

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="CIT Approved Human Genomic Sperm Library D"
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E-Coli DH10B"
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AG010124.1 GI:3294400
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Homo sapiens genomic DNA, 21q region, clone: f2G2X4, genomic survey
sequence.
AG010132 AG003943
AG010132.1 GI:3294408
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HS_2109_Al_AQ8_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2109 Col=15 Row=A, genomic survey
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                                    Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 686)

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Homo sapiens genomic DNA, chromosome 21q

Published Only in DataBase (1998)

2 (Dases 1 to 686)

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Direct Submission
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Score:

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RESULT 5 AQ667184

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ACCESSION VERSION KEYWORDS SOURCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthoria; Primates; Catarrhini; Hominidae; Homo.

B. 1 (bases 1 to 581)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizuki,Y., Yamashita,R., Shirota,M., and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

Gondact: Yutaka Suzuki
Department of Yarology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzukielms.u-cokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP314867 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR07276, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 AAAGATGGTCTTCTGAAGGCTAACTGCGGAATGAAAGTTTCTATTCCAACTAAAGCCTTA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="mammary gland"
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                                                                                                                                                                                                                                                                                                                                                                            372 GAATTGATGGACATGCAAACTTTCAAAGCA 401
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                   Submitted (08-JUL-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9561)
On Reb 5, 1999 this sequence version replaced gi:2760794.
AG003935: Submitted (09-Jan-1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 GGAATGAAAATTTCTCTTCCAAATAAAGCCTTAGAATTGAAGGACAGGAGAAAAAATTCTACAAA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 TTTATGAAGTATACATTATATAGTAATTATTGTGTTTCCAAACCCATTTAGCCTACCIGT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Auchi, Y., Yamanita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Institute of Madical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukiensu-Lokyo.ac.jp.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 514)
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/organism="Homo sapiens"
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     Direct Submission
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B. (Dases 1 to 582)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizukiima-Sugano, J., Nakai, K. and Sugano, S. Sequence Comparison of human and mouse genes reveals a homologous block structure in the promoter regions

L. Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Wirology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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Homo sapiens
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/clone="OFR01939"
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/cell line="OCUB-F"
/cell libe="OCUB-F"
/note="mammary gland tumor"
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328 GAATTGATGGACATGCAAACTTTCAAAGCA 357
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Extractors Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 582)

2 1 (Dases) 1 to 582)

3 suzuki, Y., Yamashira, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

8 squence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

1 Contact: Yutaka Suzuki

Contact: Yutaka Suzuki

Department of Virology

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Email: ysuzuki@ims.u-tokyo.ac.jp.

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BP313436
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/clone lib="Sugano CDNA library, mammary gland OCUB-F"
/note="mammary gland tumor"
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
A-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Euthoria; Primates; Catarrhini; Hominidae; Homo.

B. (Dases I to 582)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

L. Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukielms.u-tokyo.ac.jp.
Location/Qualifiers
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1 (Dases 1 to 582)

Suruki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous Genome Res. 14 (9), 1711-1718 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="mammary gland"
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/note="mammary gland tumor"
                                                                                                                                                                                                                                                                                    Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Sirockanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims_u-tokyo.ac.jp.
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cDNA clone OFR07766, mRNA sequence.
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E 1 (bases 1 to 582)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizuki, Y., Yamashita, R., Shirota, M., and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

L Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukidaina.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                          BP314260 Sugano cDNA library, mammary gland OCUB-F Homo sapiens cDNA clone OFR05703, mRNA sequence.
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BP314260.1 GI:52243235
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Homo sapiens (human)

Homo sapiens (human)

Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

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Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizubihma-Sugano, J., Nakai, R. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous Genome Res. 14 (9), 111-1718 (2004)

Contact: Yutaka Suzuki
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